



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 190795

TO: Ruixiang Li
Location: rem/4D59/4C70
Art Unit: 1646
Wednesday, May 31, 2006
Case Serial Number: 10/619992

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian (ASRC Aerospace)
STIC Biotech/Chem Library
(571)272-4161

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78733

190795

112

STIC-Biotech/ChemLib

From: Li, Ruixiang
Sent: Tuesday, May 23, 2006 9:19 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application No.10/619,992

Please do a standard search on:

SEQ ID NO: 2 against interference amino acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D59
Mail Box 4C70
(571) 272-0875

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2006, 12:48:33 ; Search time 35 Seconds
(without alignments)
2978.542 Million cell updates/sec

Title: US-10-619-992-2

Perfect score: 6215
Sequence: 1 MPVOAQMTEFLSCPTCYNE.....MSKDNDLKPVANGKMNVS 1191

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5-COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6-COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7-COMB.pep:*
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6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE-COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6215	100.0	1191	2	US-09-921-099A-2
2	6207	99.9	1191	2	US-09-921-099A-4
3	843	13.6	1048	2	US-09-921-099A-11
4	611	9.8	522	2	US-10-104-047-3665
5	194	3.1	2185	2	US-09-854-856-36
6	194	3.1	2185	2	US-10-010-720-36
7	194	3.1	2245	2	US-09-854-856-4
8	194	3.1	2245	2	US-10-010-720-4
9	194	3.1	2245	2	US-09-854-856-34
10	194	3.1	2245	2	US-09-854-856-34
11	194	3.1	2382	2	US-09-854-856-2
12	194	3.1	2382	2	US-10-010-720-2
13	193.5	3.1	1939	2	US-09-854-856-48
14	193.5	3.1	1939	2	US-10-010-720-48
15	193.5	3.1	1999	2	US-09-854-856-16
16	193.5	3.1	1999	2	US-10-010-720-16
17	193.5	3.1	2076	2	US-09-854-856-46
18	193.5	3.1	2076	2	US-10-010-720-46
19	193.5	3.1	2136	2	US-09-854-856-14
20	193.5	3.1	2136	2	US-10-010-720-14
21	193	3.1	1911	2	US-09-854-856-64
22	193	3.1	1911	2	US-10-010-720-64
23	193	3.1	1971	2	US-09-854-856-32
24	193	3.1	1971	2	US-10-010-720-32
25	193	3.1	2048	2	US-09-854-856-62
26	193	3.1	2048	2	US-10-010-720-62

27	193	3.1	2108	2	US-09-854-856-30	Sequence 30, App1
28	193	3.1	2108	2	US-10-010-720-30	Sequence 30, App1
29	193	3.1	2179	2	US-09-949-016-8129	Sequence 8129, App1
30	189	3.0	1323	2	US-09-248-796A-19543	Sequence 19543, App1
31	188	3.0	827	2	US-09-248-796A-17307	Sequence 17307, App1
32	187	3.0	2157	2	US-09-854-856-52	Sequence 52, App1
33	187	3.0	2157	2	US-10-010-720-52	Sequence 52, App1
34	187	3.0	2217	2	US-09-854-856-20	Sequence 20, App1
35	187	3.0	2217	2	US-10-010-720-20	Sequence 20, App1
36	187	3.0	2294	2	US-09-854-856-50	Sequence 50, App1
37	187	3.0	2294	2	US-10-010-720-50	Sequence 50, App1
38	187	3.0	2354	2	US-09-854-856-18	Sequence 18, App1
39	187	3.0	2354	2	US-10-010-720-18	Sequence 18, App1
40	182.5	2.9	4019	2	US-09-854-133-425	Sequence 425, App1
41	182	2.9	2004	2	US-09-854-856-58	Sequence 58, App1
42	182	2.9	2004	2	US-10-010-720-58	Sequence 58, App1
43	182	2.9	2032	2	US-09-854-856-42	Sequence 42, App1
44	182	2.9	2032	2	US-10-010-720-42	Sequence 42, App1
45	182	2.9	2064	2	US-09-854-856-26	Sequence 26, App1

ALIGNMENTS

RESULT 1

US-09-921-099A-2
; Sequence 2, Application US/09921099A
; Patent No. 6602707
; GENERAL INFORMATION:
; APPLICANT: Heffeneider, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bernette, Robert
; APPLICANT: Seiss, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene at
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/09/921, 099A
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-921-099A-2

Query Match 100.0%; Score 6215; DB 2; Length 1191;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MPVOAQMTEFLSCPTCYNEFPDENVHKPISLGCSTHVCTCKLNRKACPPDQTAINMD	60
DB	1	MPVOAQMTEFLSCPTCYNEFPDENVHKPISLGCSTHVCTCKLNRKACPPDQTAINMD	60
QY	61	IVLPVNFALDLVGAQVDPDHOSIKLSNLDENKHYEVAKKVEDLALTYLKPSGKGVAS	120
DB	61	IVLPVNFALDLVGAQVDPDHOSIKLSNLDENKHYEVAKKVEDLALTYLKPSGKGVAS	120
QY	121	LNQSAISRMPQKRLVTVNCOQVEEGRVRAARASLIGERTVTELLIHOHQOQSANI	180
DB	121	LNQSAISRMPQKRLVTVNCOQVEEGRVRAARASLIGERTVTELLIHOHQOQSANI	180
QY	181	MAAVNRAGCGFPGPMOEFALKLVLLALPDGALSRSKVLPVVOQLERFPQASTSIG	240
DB	181	MAAVNRAGCGFPGPMOEFALKLVLLALPDGALSRSKVLPVVOQLERFPQASTSIG	240
QY	241	HVVOLLRYASCPKVTGRDESSIMOLKEFRSEYALRRHDAQIVHIAEAGLRISPEQW	300
DB	241	HVVOLLRYASCPKVTGRDESSIMOLKEFRSEYALRRHDAQIVHIAEAGLRISPEQW	300
QY	301	SSLLYGLDAHKSHMOSIIDKLOSPEFAKSVQVELTIVLORTGDPANLNLRLPHELLANI	360
DB	301	SSLLYGLDAHKSHMOSIIDKLOSPEFAKSVQVELTIVLORTGDPANLNLRLPHELLANI	360

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OY 361 DENPDVAVSPTWEOLENAMVAVKTVVHGLVDFTIONYSRKGHETPOPOPNKSKYKTSKCRDLR 420
DB 361 DENPDVAVSPTWEOLENAMVAVKTVVHGLVDFTIONYSRKGHETPOPOPNKSKYKTSKCRDLR 420
OY 421 OQGGCGRGNTCTFAHSQOELEKYLRLNKKINATVTRTPEPLNKVGVNNVTTTAGNVISYI 480
DB 421 OQGGCGRGNTCTFAHSQOELEKYLRLNKKINATVTRTPEPLNKVGVNNVTTTAGNVISYI 480
OY 481 GSTETTTGKIVPSTNGISNAENSVSOLISRTSDSTLRALTEVTKVGVGVANGONGNAAPSDAD 540
DB 481 GSTETTTGKIVPSTNGISNAENSVSOLISRTSDSTLRALTEVTKVGVGVANGONGNAAPSDAD 540
OY 541 SYTENKIGSPKTPVSNVATASAGPSNVGTELSVPQKSSPFLTRPVYVPPHSENIQYRQ 600
DB 541 SYTENKIGSPKTPVSNVATASAGPSNVGTELSVPQKSSPFLTRPVYVPPHSENIQYRQ 600
OY 601 DPTQIPEFVPOYPOTGYVPPPTVAGVAPCVPRFVRNNVPESSLPPASMPYADHYST 660
DB 601 DPTQIPEFVPOYPOTGYVPPPTVAGVAPCVPRFVRNNVPESSLPPASMPYADHYST 660
OY 661 FSPDRMNSSPYQPPPOYGPVPPVPSGMVAPVYDSRRIWRPMTQRDDIIRSNLSLPM 720
DB 661 FSPDRMNSSPYQPPPOYGPVPPVPSGMVAPVYDSRRIWRPMTQRDDIIRSNLSLPM 720
OY 721 DVHSSVYQTSLRERNISLDGYYSVACOPPESEPTVPLPREPCGHLKTSCEQIRKPD 780
DB 721 DVHSSVYQTSLRERNISLDGYYSVACOPPESEPTVPLPREPCGHLKTSCEQIRKPD 780
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DB 781 QMAQYHTQKAPLVSSSTLPVATOSPTPSPPLFSVDFRADSESISGTFEEDHLSHSPMS 840
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DB 841 CGTIGSCINAIIDSEPKDVANSNAVIMDLDSGDVKRVLHFEORTKXEDPIIPSPDGP 900
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DB 901 IISKWGAISRSRSTGYHTTDPVQATASQGSATKPIISVDYVPVYVNAVDSRMSYGNPEATS 960
OY 961 SAHYVERDRPIYTDLSGHRKHSSTGDLLELOAKSNSLLQREANALAMQOKMSLDB 1020
DB 961 SAHYVERDRPIYTDLSGHRKHSSTGDLLELOAKSNSLLQREANALAMQOKMSLDB 1020
OY 1021 GRLTLNLSKTELKNGELSDYTEDADDTKPDRIELELSALDDEPQOSEPIEELI 1080
DB 1021 GRLTLNLSKTELKNGELSDYTEDADDTKPDRIELELSALDDEPQOSEPIEELI 1080
OY 1081 DIQLGISQNDQILNMAVENGHPVOOHOKEPKOKKOSIGEDHVLLEBQKTLIPYTSGF 1140
DB 1081 DIQLGISQNDQILNMAVENGHPVOOHOKEPKOKKOSIGEDHVLLEBQKTLIPYTSGF 1140
OY 1141 SQPLPVISINASCPIITTSVSAGNLLIKTHVMSXNDPLKPYANGKMS 1191
DB 1141 SQPLPVISINASCPIITTSVSAGNLLIKTHVMSXNDPLKPYANGKMS 1191

RESULT 2
US-09-921-099A-4
; Sequence 4, Application us/09921099A
; Patent No. 6602707
; GENERAL INFORMATION:
; APPLICANT: Hefeneider, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seiss, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/09/921, 099A
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4

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; LENGTH: 1191
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-921-099A-4
Query Match          99.9%; Score 6207; DB 2; Length 1191;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MVOQAQWTEFLSCPICVNEPDENVHKPISLCSHTVCKCLNKHAKACPDQQTINMD 60
DB 1 MAVQAQWTEFLSCPICVNEPDENVHKPISLCSHTVCKCLNKHAKACPDQQTINMD 60
OY 61 IDVLVYNFALLQVGAQVDPDHSIKLSNIGENKHYEVAKKCEVDLALYLKPSGGKGVAS 120
DB 61 IDVLVYNFALLQVGAQVDPDHSIKLSNIGENKHYEVAKKCEVDLALYLKPSGGKGVAS 120
OY 121 LMQSALSRPMQKRLVTLVNCQLVEEGRVRAARAARSLGERVTTELILQHQNPQOLSANL 180
DB 121 LMQSALSRPMQKRLVTLVNCQLVEEGRVRAARAARSLGERVTTELILQHQNPQOLSANL 180
OY 181 MAVBARCGQFLGPMQOEALKVLVLLALPDGALSARKVLVFLVQRLERFPQASTISIG 240
DB 181 MAVBARCGQFLGPMQOEALKVLVLLALPDGALSARKVLVFLVQRLERFPQASTISIG 240
OY 241 HVOQLLYRASCFKTKRKDEDSLSMOLKEBFRRSYEALRREHDAQIVHIAEAGLRISPEQM 300
DB 241 HVOQLLYRASCFKTKRKDEDSLSMOLKEBFRRSYEALRREHDAQIVHIAEAGLRISPEQM 300
OY 301 SELLVGDILAHKSHMOSIIDKLOSPEFAKSVQELTIVLORTDPPANLRLRPHLELLANI 360
DB 301 SELLVGDILAHKSHMOSIIDKLOSPEFAKSVQELTIVLORTDPPANLRLRPHLELLANI 360
OY 361 DENPDVAVSPTWEOLENAMVAVKTVVHGLVDFTIONYSRKGHETPOPOPNKSKYKTSKCRDLR 420
DB 361 DENPDVAVSPTWEOLENAMVAVKTVVHGLVDFTIONYSRKGHETPOPOPNKSKYKTSKCRDLR 420
OY 421 OQGGCGRGNTCTFAHSQOELEKYLRLNKKINATVTRTPEPLNKVGVNNVTTTAGNVISYI 480
DB 421 OQGGCGRGNTCTFAHSQOELEKYLRLNKKINATVTRTPEPLNKVGVNNVTTTAGNVISYI 480
OY 481 GSTETTTGKIVPSTNGISNAENSVSOLISRTSDSTLRALTEVTKVGVGVANGONGNAAPSDAD 540
DB 481 GSTETTTGKIVPSTNGISNAENSVSOLISRTSDSTLRALTEVTKVGVGVANGONGNAAPSDAD 540
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DB 541 SYTENKIGSPKTPVSNVATASAGPSNVGTELSVPQKSSPFLTRPVYVPPHSENIQYRQ 600
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DB 661 FSPDRMNSSPYQPPPOYGPVPPVPSGMVAPVYDSRRIWRPMTQRDDIIRSNLSLPM 720
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DB 781 QMAQYHTQKAPLVSSSTLPVATOSPTPSPPLFSVDFRADSESISGTFEEDHLSHSPMS 840
OY 841 CGTIGSCINAIIDSEPKDVANSNAVIMDLDSGDVKRVLHFEORTKXEDPIIPSPDGP 900
DB 841 CGTIGSCINAIIDSEPKDVANSNAVIMDLDSGDVKRVLHFEORTKXEDPIIPSPDGP 900
OY 901 IISKWGAISRSRSTGYHTTDPVQATASQGSATKPIISVDYVPVYVNAVDSRMSYGNPEATS 960
DB 901 IISKWGAISRSRSTGYHTTDPVQATASQGSATKPIISVDYVPVYVNAVDSRMSYGNPEATS 960

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QY 961 SAHYVERDFITVLSGHRKHSSTGDLSTLELOQAASNSLLQREANALAMQKMSLDE 1020
DB 961 SAHYVERDFITVLSGHRKHSSTGDLSTLELOQAASNSLLQREANALAMQKMSLDE 1020
QY 1021 GHHLTLNLKSKEIELANGELQSDYTEDADITKPDRIEIELSALDTEDEPGOSEPIEELI 1080
DB 1021 GHHLTLNLKSKEIELANGELQSDYTEDADITKPDRIEIELSALDTEDEPGOSEPIEELI 1080
QY 1081 DTQLGSSONDOLINGMAVENGHVVOOHQKEPPKQKQSLGEDVHLEEQKTLTPVTSCEP 1140
DB 1081 DTQLGSSONDOLINGMAVENGHVVOOHQKEPPKQKQSLGEDVHLEEQKTLTPVTSCEP 1140
QY 1141 SGPPLPVSISNASCLPTTTSVSAGNLLKTHVMSSEKNDPLKPVANKMNS 1191
DB 1141 SGPPLPVSISNASCLPTTTSVSAGNLLKTHVMSSEKNDPLKPVANKMNS 1191

RESULT 3
US-09-921-099A-11
Sequence 11, Application US/09921099A
Patent No. 6602707
GENERAL INFORMATION:
APPLICANT: Hefeneider, Steven
APPLICANT: Merkins, Louise
APPLICANT: Bennett, Robert
APPLICANT: Seiss, Donald
TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
FILE REFERENCE: 00-617-A
CURRENT APPLICATION NUMBER: US/09/921, 099A
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 1048
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-921-099A-11

Query Match 13.6%; Score 843; DB 2; Length 1048;
Best Local Similarity 30.6%; Pred. No. 4, 3e-59;
Matches 238; Conservative 99; Mismatches 278; Indels 162; Gaps 23;

QY 4 QAAMWTEFLSCPTCYNEPDENHAKPISLGSHTVCTCLNKLHR--KACPFQDTAINTDI 61
DB 6 QGGQWQEVLCSSICNRHENE-TFLPVSLICGHVTCCKCAEKPENQTKPCPHDWMKTTSP 64
QY 62 DVLPVNFALLQVGAQVPDHQSIKLSNLGENKHVEYAKKCVEDLALYLKPLSGKGVASL 121
DB 65 SEYPPNNVALLSVI---FPRKQCMTSLSGAVSEAKRYDLSIQ-TAKFPREADSERG-GTV 119
QY 122 NOSALSRPWQKRLVTLVNCQVLEEGRVAMRAARSLGERTYTELLILOHQPQOLSANIM 181
DB 120 SSREISRTLOKRLKVALCYQWREVDGRLKTKMKRCGISERVMETILISQSTHVSQLM 179
QY 182 AAVRARGCOFLPAMOEALKVLALLEDGSAISRKYVLFVQVRLERPPFPAQKSTISGH 241
DB 180 SAVRARGCOFLPAMODVLRLLMLLETGECIARKNLVMYVQTILASDYPQVSKTCVGH 239
QY 242 VVQLLYRASCFCYTKRDEDSLMQLKEEPRSYEARERHDAQIVHAMEAGLRISPEQMS 301
DB 240 VVQLLYRASCFCYTKRDEDSLMQLKEEPRSYEARERHDAQIVHAMEAGLRISPEQMS 301
QY 302 SLIYGLDLAKHSMQSIIDKLQSPESFAKSVQELTIVLORTGDPAN-----LNRLRP 352
DB 300 ALLYVADQSHRSHMQSIIDKLQSGNSYQGVVEELRAL---AGSQTSMVLAAYRYFLTVLP 356
QY 353 HIELLANTIDPNDAVPTMEOLEMANVAVKTVHGVLDPIQNY---SRGHEPRPQQRMS 409
DB 357 CLEFFGIIHEHTSMIGIDALHQRILTK--LHSCQDDLRKMPKEERKGVILLQAEVPGG 414
QY 410 KYKTSKCRDLROOGGCGPRTNCTFAHSOBELEKYRLRNKKINATVTPFLNKKVGNNTV 469
DB 415 -----MGGPGGSG-----GAFAGR----- 430

QY 470 TTAGNVISVIGSTETTGKIVPSTNGISNENSVSGLISRSIDSTLRALETVKKVGVGA 529
DB 431 -----GGHLPYSQIDETGSRISRTNPKDMSHSPO----- 461
QY 530 NGONNAGPESADVTEKIKSPKPTPVSNVAATSAGPSNVGTELSVPKSSPFLTRVPVY 589
DB 462 -----TPPKQPRQKRYQMGIPRNKNG-----YSSDAPPIPSHQOQ 497
QY 590 PPHSENIOYQDPRTQIPEVPOYPOTGYYPPPPVPAVACVPRFVSNVNESSLPP 649
DB 498 PPP-----QEFNS--QHLPQRFGRGQRGAPPPPPPP-----MPLIGVD-----MFG 539
QY 650 ASMPYADHSTSPDRMNSP-----YQPPPPQPIGPVPPVPSGMYAIVYDSRRIWRP 704
DB 540 APMQATEVLT-ADQMVNGTQRVVMQSPFHLPGGPVVMIPQOQVPPPOSMTPEVGP 598
QY 705 MYQRDDIIRSNGLPPMDVHSSV-YQTSLERYNSLDGYSV---ACOPPEPRTTV 757
DB 599 M-----GPMGPMTPSIPVQVPPNTMTATSPGVSIVYPAASFPQGPHTI 643

RESULT 4
US-10-104-047-3665
Sequence 3665, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTIYTUTE
TITLE OF INVENTION: No. 6943241el full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104, 047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3665
LENGTH: 522
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-3665

Query Match 9.8%; Score 611; DB 2; Length 522;
Best Local Similarity 34.1%; Pred. No. 1e-40;
Matches 187; Conservative 76; Mismatches 187; Indels 98; Gaps 27;

QY 618 YTPPPTVAGVAPCVPRFVRSNVPESSLPASMPYADHYSTFSPDRMNSPYQPP 677
DB 2 YTPPP-----QCYSRFR-----PPSAPBPAPYLDHYPPYL-QERVANSQYGTQ 49
QY 678 QPYGVPVPSGMYAPVYDSRRIWRPMYQDDIIRSNGLPPMDVHSSV--YQTSLE 735
DB 50 Q-----YPPI-----YPSHYDGRVYPAFSYTRREIFESP1-DLEIPRAVPSPVPSR 100
QY 736 YNSLDGYVACQ-----PS-----EPRTVPLPRECGHLKTSCEQIRKQDQMYNHT 787
DB 101 YQIISYVPVAPHPQIRPSYLRBPYSRLPPQ---HPSLDLHRRKREIMQLEB 156
QY 788 QKAPLVSTLPVATOSPPTPSPFLFSVDFRADSESYSGTKEFEDHLSHPMSCGTIGSC 847
DB 157 RK---VISPPPPA-PSPTLP-PTFHPEEFLDDDLAVAG-KYKGNDSQSPMSCDITGSV 210
QY 848 INAIDSEPKDVANSNAVIMLIDSGDVKRRVHLEFQRTKE--EDPIIPFSDGPIISKV 905
DB 211 IGTKAKPQDVVAAGSVEEMANVESKGM--RDQRLDQRAAETSDDLLIPFGDRPTVSRF 268
QY 906 GAISRSRPGYHTTDPVQATASQGSATKPISVDPVYVNAVDSRW--SSYG--NEATSS 961
DB 269 GAISRTSKTIYQAGBPQAMAPQGAFTKINSIDSPI--GTHGNGASPIYSHQNIIPQ 326
QY 962 AHYVERDFITVLSGHRK--HSSTGDLSTLELOQ-----AKNSLLQ 1004
DB 327 GHFSERERISMESVASHGKFLPSAREQRLLELOQNHQISOOTQLRGPEAVSNRLVLR 386

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QY 1005 EANALAMQ-----KXNSLDEGRHLTLNL--LSKETELANGELQSDYTEADATDKPD 1054
Db 367 EANTLAGSQPPPPPPKPMISBOULSELHVOERELGKRTRELSME--NOCSLDMK-- 443
QY 1055 RDIELELSALDTE--PDGQSEPIEIBLDIOGLISSONDOLINGMAVENGHVPVOOHQKBP 1112
Db 444 -----SKLNTSKAENGQPEPKV-----PAEDLTLTFSDPVPRGSLTQJENISL 488
QY 1113 PKQKQSL 1120
Db 489 LSNKTSLSL 496

RESULT 5
US-09-854-856-36
; Sequence 36, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Made
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 2185
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)---(2185)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-36

Query Match 3.1%; Score 194; DB 2; Length 2185;
Best Local Similarity 18.5%; Pred. No. 1e-05;
Matches 235; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

QY 48 KACPDDQTAINT-----DIDVLFNFAIIQVLGAVQVPHOSTGLSLNGEN 92
Db 315 KRASFSAKSVIGTPEFMAPEMEYERKYDESVDVYAFGCMLEMATSEYP----- 361
QY 93 KHYEVAKKQVEDLALVLKLSGGKGVASINQSAL-----SRPMQKCLVTLVN 139
Db 362 -----YSECQNAQIYRRVTSQVK--PASFDKVAIPVKEIIBGCCIRONKDERYSIDOLIN 415
QY 140 COLVEBEGVRAMRAARSLSGERTVELLIIOHONPOOLSANLMAAVARAGQFLGPAMOE 199
Db 416 HAFQGETGVRLVLAEBDDQEKAIKLMWRIEDIKKLK-----GKKXKME 460
QY 200 ALKLVLLALEDGALSRLKVLVLFVQRLBRRPPOASKTSIGHVQULLYRASCFKVTKRDE 259
Db 461 AIEF-----SFDLBRDVEDVAQEMVESGYVCEGDHKTMAKAIIDR-- 501
QY 260 DSSIMQLKEFRFEYALRRBHDAQIYHIMEAGLRISPEQMSLLYGLDLAKHSMQSIID 319
Db 502 -VSLIRKKEOR--QLVREOEKK-----KQESSLSLQOQVQSSASQGTJK 544
QY 320 KLASPESFAKSVDELTVLQRTDP-----ANLNRLRPHLELANTIDPNDAVSPTW 371
Db 545 QLPASATGIPATASTASVSTOVEBEPADQHQOQYQCPSTSVLS--DGTVDSSQGS 602
QY 372 EOLENAMAVKTVVHGLVDFIQNYSRKGHET-----PQOPNYSKYTSMCRDL 419
Db 603 VFESHVSQQTIVSYG-----SQHQAHSHTGVPGHIBSTVQAOSQPHGVVPPSSVAQG 656

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QY 420 ROQGCPRGINTCTFAHSGOEBLEKYLRLNKKINATVTRFPLLNKGVNNVTITAGNVISV 479
Db 657 QSQGQ--PSSSLTGVSSSQPIQHPO-----QQQGIQOTAPRQ----- 692
QY 480 IGSTETTGKIVSTNGISNAENSVSQILSRSTDSLRALETYKVKVKGVCANGAQNAAQPEA 539
Db 693 -----QTVQYSLSQ--TSTSSEAT-----TAQVPVSOPOA 719
QY 540 DSVTENKIGSPKTPVSNVAATSAGPSN--VGTELNSVPQKSSPFLTRY-----PVVPP 591
Db 720 PQVLP-QVSAQKQLVSPQVPTIQGBPOI PVATQPSVVPVHSGANFLPVQPLPTPLDP- 777
QY 592 HSENIQVODPRQTIPEFVPOY--PQTGYPPPTVPAGVAPCBVPRFVSNVNPSSSLP- 648
Db 778 -----QYVSOQPISTPHVSTAQGTGSSLPITMAAGITQ--PLUTLASSATTAATIG 827
QY 649 -----PASMPYADHSTSPRDRMNSSPY-----QPPP-----PQYGVPPVPVSGMYAV 694
Db 828 VSTVPSQLP-----TLQPVTLQPSQVHPQLQCPAVQSGMGI PANLQGAAYEPLSSGDVL 882
QY 695 YDSRKIMRPMTQRDDIIRSNLSLPRMDVHSGSVYQTSLRERNNSLDGYVSVAQOPSEBR 754
Db 883 YGQFPFRLPPOYRGDSNIAPSSNVASVCIHSTVLXPMTETVALTPGYFPVVOQPVESN 942
QY 755 TVPL-----PREPCGHL-----KTSCEBOIRKKPDQMAOYHTQKAPLVSTLPLVATO 802
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QY 803 SP--TPSPPL-ESVDF-----RADFSEBVSQKFEEDHLSHYS PWSCGTITGCINAI 851
Db 995 QPOATQPTLASSVNSASHDVNASGMSDGENENPSSSGRHEGRTTKKHVKSYSRSRHRK 1054
QY 852 DSEPKDVIAN-----SNVLMDLDSGDVYK&VHLFETQRTKEBPDIIPSPDPIISKMG 906
Db 1055 TSPRKRLILNVSNGKDRVVECOLETHNRKMVTFPKDLDGDNBEIATITVNNDFIL---- 1110
QY 907 AISRSS-----RTGYHTDPVQA-----TASQ--GSATKP 934
Db 1111 AIERESFVQVQVEIIEKADMLESDVSVRBDQGLIESIQGMDVDFSSQKLEGFQKP 1170
QY 935 ISVSDVVPYVNAVDSRWSSYGNBATSAAHYVERDRFIYVTLDSGHRHSG--TGDL--SL 990
Db 1171 IPASSMPQOIGIPTS-----SLTQVHVSAGR--RFTVSPVESRLRESKVPPESEITDV 1222
QY 991 ELQQAQKNSLLIQREANALAMQKXNSLDBGNHLTLNLKSELBELNGELQSDYTEADAT 1050
Db 1223 AASTAQSPKMNLSHSHASSLSLQOAFS-----ELRRQW--TEGPNT 1261
QY 1051 TKPRRD-----IELELSALDTEPDGQSEPIEIBLD--IOLGISQONQ 1092
Db 1262 APPNFSGHTPTFPVPPFLSTIAGVPTTAATAAPVATSSPNDISTSVIQSEVTVPTBE 1321
QY 1093 LINGMAVENGHVPVOOHQKBPPOKQKOSLGBDHVILEQKTLIPVYSCFQOPPLVSIANS 1152
Db 1322 GIAGVASTGVVTSQGLPIPP-----VSESFVLSVSVSITIPAVVSISTS 1368
QY 1153 -CLPITTSVS 1161
Db 1369 PSLQVPTSTS 1378

RESULT 6
US-10-010-720-36
; Sequence 36, Application US/10010720
; Patent No. 6858419
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Made
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hansen, Gwenn
; APPLICANT: BeltrandeRio, Hector

```


APPLICANT: Van Sligtenhorst, Isaac
TITLE OF INVENTION: No. 6858419el Human Kinases and Polynucleotides
FILE REFERENCE: Encoding the Same, And Uses Thereof
CURRENT APPLICATION NUMBER: US/10/010,720
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/206,015
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/854,856
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 2185
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(2185)
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-010-720-36

Query Match 3.1%; Score 194; DB 2; Length 2185;
Best Local Similarity 18.5%; Pred. No. 1e-05;

Matches 225; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

48 KACPDPQAINI-----DIDVLFNFIQLVGAQVPHQSIKLSLGEN 92
315 KASFAKSIYIGTFEAPMEYEKYDESVDYAFGCMLEMAISEYF----- 361
93 KHYEVAKKVEDLALVTLKLSGKGVAISLNSAL-----SRPMOKLVTLVN 139
362 ----VSECQNAQIYRRTYSGVK-PASFDKVAIPVKEIIEGCRIRONDERYSIDOLN 415
140 COLVEEGVRAMARASLGEFRTVELIHOQNPOLSAIWAARAGCOFLGPMOEE 199
416 HAFPOEITGVRLAEEDDEGKAIKLMRIEDIKLK-----GKKKME 460
200 AKLVLLLEDGSAISRKVLVLFVORLEPRPQASKISGHVQLLYRASCFTVKRDE 259
461 AIEF-----SFLERDVPEVAQEMVESGYCEGDHKTMAKAIKDR-- 501
260 DSLIQLKEEPRSYEALREHDAQIVHIMENGLRISPPOMSLYGLDLAKHSHMOIID 319
502 -VSLIKRKEQR-QLVREEQEK-----KQESSIKQOYEGSSASQTK 544
320 KLOSPEFAKSVQELTIVLQRTGDP-----ANLRLRPHLELLANIDPNDVSPTW 371
545 QLPASASTGIPASTSASVSTQVEPRERADQHQLOQOQPSISVLS--DGVDSGQSS 602
372 EOLENAAVAKTVVHGLVDFIQNYSKKHET-----PQOPNSKYKTSKCRDL 419
603 VFTESVSSQOQVSYG-----SQHEQASHGTVPGRHIPSTVOAQOQPGHVVPPSSVAQ 656
420 RQGGGPRRTNCTFPAHSELEKRYLRANKKIATVTFPLMKVGNNTVTAGVIV 479
657 QSQGQ-PSSSSLGVSSQPIQHPQ-----QQGQIQTAAPQ----- 692
480 ISETETGKIVSTNGISNAENSVSQILSRSTDSTLRALETYAKVKGKVGANGAAGPSA 539
693 -----QTVQYSLSQ-TSTSEAT-----TQPVSGQQA 719
540 DSVTEHKISPPKTVSNVAATSAGPSN--VGTSLNSVPQKSSPFLTRY-----PVYPP 591
720 PQVLP-QVSAQKQLPVSPQVPTIOGEPQIPIVATQPSVNVHNSGHNFLPVGQPLPTLP- 777
592 HSENIQVDPDRTPQIFEVPRQV--PQTGYRRPRTPARACVAPCVRFVANSNNPESSLP- 648
778 -----QYVSQLPISITPHVSTAQTGFSSLPITAAAGITQ--PLTLTASSATTAAITG 827
649 -----PASPVPADHSTFSPDRMNSSPY-----PQPVGPVPVPVPSGMYAPV 694
828 VSTVPSQGP-----TLQPVTVQQLPQGVNHPQLLQFVAVSGMGRANLNGAABEVLLSSGDVL 882

QY 695 YDSKRIWRPMPYQRDDIIFSNLSIPMDVWMSVYQTSLEERYNSLDGYYSVACQPPSEPR 754
DB 883 YQGFPRPLRPQYRGSNLAAPSSNVASVCHSTVLRPMTEVLATRGYPPTVQPVESN 942
QY 755 TTVPL-----PREPCGL-----KTSCEQIRRKRPDQMAQYHTQKALVSSLTLPVATQ 802
DB 943 LVPVKGVGQVQVSPGSLAQAPTTSSQAVLES-----TQGVQVAPAEVAVYA 994
QY 803 SP--TPSPPL-FSYDF-----RADFSESVSGTKFEBDHLSHSPMSCGTTGSCINAI 851
DB 995 QQAATQPTTLASSVDASHDVASGMSDGNENVPSSSGRHEGRTYKHYKYSVRSRHEK 1054
QY 852 DSEPKDVIAN-----SNALMDLSDGVYRRNHLFTQRTKREEDPIIFSPGPIISKMG 906
DB 1055 TSPFKRLILNANSGKDRVVECOLETHNRKMTFKFDLGDNDPELATIWNDFIL---- 1110
QY 907 AISRSS-----RTGYHTDPVQA-----TASQ---GSATKP 934
DB 1111 AIERESFVQVAREIIEKADBLESDVSVEPRBDQLESIQKDDYGFSSQKLEGEFKQ 1170
QY 935 ISVSDVVPYNAVDSRWSYGNBATSSAHYVERDRPIVTDLGHRHSS--TGDLI-SL 990
DB 1171 PASSWPQIGIPTS-----SLTQVVAHAGR-RTVGPVPSRRLRESKVPFSRITDVY 1222
QY 991 ELQAKNSLLLOREANALAMQKNSLDRGHLITNLKSELANGELQSDYTEDAD 1050
DB 1223 AASTQSPQPMNLSSHASSLSIQAFS-----ELRRQM---TEGPNT 1261
QY 1051 TKPRDR-----IELESLADTIDEPDQSEPIEIID--IQLGISQNDQ 1092
DB 1262 APPNFSHTGTPPVVPFPLSSIAQVPTTAAATAPVATISSPRDISTSIVQSVYPTPE 1321
QY 1093 LUNGAIVENGHVQOQKPPKQKQSLGBDHVILEEQITLIPVTSFSGOPLVPSISNAS 1152
DB 1322 GIAGVATSTGVVTSGLPIFP-----VESPVLSVSVSITPRAVSIISTS 1368
QY 1153 -CLPITTSVS 1161
DB 1369 PSLQVPTSTS 1378

RESULT 7

US-09-854-856-4
Sequence 4, Application US/09854856
Patent No. 6541252
GENERAL INFORMATION:
APPLICANT: Walke, D. Made
APPLICANT: Hilbun, Erin
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
FILE REFERENCE: Encoding the Same
CURRENT APPLICATION NUMBER: US-0178-USA
PRIOR FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 60/206,015
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 2245
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(2245)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-4

Query Match 3.1%; Score 194; DB 2; Length 2245;
Best Local Similarity 18.5%; Pred. No. 1.e-05;
Matches 225; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

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QY 48 KACPEDQTAINT-----DIDVLPVNFALLQVAGVPHDQSTIKLSNUGEN 92
DB 375 KRASFAXSVIGPPEFMARPEMYEEKYDESDVYAFGCMLEMAATSEYP-----421
QY 93 KHVEAKKCCVEDLALYLKPLSGGKVASLNOGAL-----SRPMQRKLVTLVN 139
DB 422 -----YSECONNAQIYRRVTSGVK--PASFDKVAIPEVKEIIEGCI RÖNNDERYSIKDLIN 475
QY 140 COLVEEGRVAMRAARSIGERTVTELLIOHONPOOLSANLMAAARACQQLGPMQOE 199
DB 476 HAFFOETGVRLVELEEDDEKAIKLMWRIEDIKLK-----GKYKNE 520
QY 200 ALKVLVLALEDGALSARKVLVLFVVQRLBPRFPQASKSIGHVOLLYPASCFTVKRDE 259
DB 521 AIEF-----SFDLERDVPEDVAQEMVSGYVCEDDHKTMAKAIKDR--561
QY 260 DSSLMOQLKEEFSYEALREHDAQIVHIMEAGLRISPQWSSLLYGLDLAKSHMQSIID 319
DB 562 -VSLIKRKEOR--QVREEOEKK-----KQESSLKOQVEQSSASQGTIK 604
QY 320 KIQSPESFAXSVQELTYVLTQRTGDP-----ANLNRLRPHLELLANIDPNPDVSPW 371
DB 605 QLPASASTGTPTASTTSASVSTQVEEPRADQHOLOQOQPSISVLS--DGTVDSCQSS 662
QY 372 EGLNAMVAVKTVHGLVDFIONYSRKGHET-----POQOPSKYKTSWCRDL 419
DB 663 VTESVSVSQQIVSYG-----SQHEQANSTGVPCHITSTYQAOQOPHGVIPRSSVAQ 716
QY 420 ROQGGCPRGCTNCTFAHSGELEKYLRLNKNATVATPFLNKVGVNNTVTAGNVISV 479
DB 717 QOQGGQ-PSSSSLTGVSQPIQHPQ-----QOQGGIQRTAPQ-----752
QY 480 IOSTETTKIVSTNGCISNAENSVSQILSRSTDSTILAEITYKKVKVQANQONAGPBA 539
DB 753 -----QTVQYSLSQ-TSTSEAT-----TAQVPSQPA 779
QY 540 DSVTENKIGSPKTPVSNVAATSAGPSN--VGLMELSVPOKSPFLTRY-----PVYPP 591
DB 780 PQLVP-QVAGAKQLPISQVPTIQSEPOQPVATQPEVNVVHSGANHLPGQPLPTLLP- 837
QY 592 HSENIQYFODPRTQIPEFVPOY--PQTYGYPPTPVPAVAPCPVRPVSNNVPESSLP- 648
DB 838 -----QVPSQIPSTPHVSTAQTFSLPTMAAGITQ--PLTLASSATTAIDG 887
QY 649 -----PASMPYADHVSFTSPRDMNSPY-----QPP-----PQPYGPVPVPSGMYAV 694
DB 888 VSTVPSQLP-----TLQPVYQQLPQVHPQQLQPAVQSGMIGIPANLGOAEVPLSSGDLV 942
QY 695 YDSRRIWRPMYQORDIIRSNLSLPRMDVMHSSVYQTSLEERYNSLDGYYSVACQPESEPR 754
DB 943 YQGFPRRLPQYRGDSNIAPSNVASVCHSTYLXAPMPREVLATGCIPTTVQPIVESN 1002
QY 755 TVVPL-----PREPCGHL-----KTCSEBOIRRRPDQMAOYHTQKAPLVSTLPAVATQ 802
DB 1003 LLYPMQGVQGVQVQSGSLAQAPTTSSQOAVLES-----TQGVQVABAEVAVAA 1054
QY 803 SP--TPSPSL-PSYDF-----RADFSVSSTGTFEEDHLSHYPSMCGTIGSCINAI 851
DB 1055 QOQATOPPTLASSVDASHDVASGMSDGMENVPSSGRHGRITTKHRYKSVSRHREK 1114
QY 852 DEEPKQVIAN-----SNAYLMDLDSGDVVRVRLPFTQRTKEEDLIPSPDPIISKMG 906
DB 1115 TSBPKRIILNVSKGRVVECOLETHRRKRVTKPFDLDGDNPEIATIMNNDFIL-----1170
QY 907 AISRSS-----RTGYHTDPVQA-----TASQ-----GSATKP 934
DB 1171 ATERSEFVQVRETIKADEMLSEDSVSEPEBQOGLSLOKXDYGFSGSQKLEGFQD 1230
QY 935 ISVSDVVPVYNAVDSKMSYGNATSSAHYVERDRIYVDLSGRHSS--TGDL-SL 990
DB 1231 IPASSMPOOIGIPTS-----SLTOVHVSAGR-RFIVSVPEBSRLRESKVPEITDTV 1282

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QY 991 ELQAKSNLSLLQREANALAMQOKNNSLDEGRHLTLNLKSKEIENRGELOSYTEDATD 1050
DB 1283 AASTAGSGMNLSSHASLSLOQAS-----ELRACM-----TEGPNT 1321
QY 1051 TKPRD-----IELESLDITDEPDQSEPIEELD--IQGJSSONDQ 1092
DB 1322 APPNFSHTGTPPVVPPFLSSIAGVPTTAAAPVAPATSSPNDISTSVIOSEVTPTEE 1381
QY 1093 LINGMAVENGHVQOQHOKEPRKQKQSLQEDHVILEQKTLIPYTSQFQPLPVISNAS 1152
DB 1382 GIAGVATSTGVTTSGGLPIPP-----VSESPVLSVSSITTPAVVISITTS 1428
QY 1153 -CLPITTSVS 1161
DB 1429 PSLQVPTSTS 1438

RESULT 8
US-10-010-720-4
; Sequence 4, Application US/10010720
; Patent No. 6858419
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hansen, Gwenn
; APPLICANT: Beltrandelrio, Hector
; APPLICANT: Van Sligtenhorst, Isaac
; TITLE OF INVENTION: No. 6858419el Human kinases and Polynucleotides
; FILE REFERENCE: Encoding the Same, And Uses Thereof
; FILE REFERENCE: LEX-0382-USA
; CURRENT APPLICATION NUMBER: US/10/010, 720
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/206, 015
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/854, 856
; PRIOR FILING DATE: 2000-05-14
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2245
; TYPE: PR
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2245)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-10-010-720-4

Query Match 3.1%; Score 194; DB 2; Length 2245;
Best Local Similarity 18.5%; Pred. No. 1,1e-05;
Matches 225; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

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QY 320 KLQSPESPAKSVQELTIVLQRTGDP-----ANLNRLRPHLELLANIDPNDVSPW 371
DB 605 QLPASASTGIPYASTTSASVSTQVEEPEPADQHOQLQYQOQPSISVLS--DGTVDSCQGS 662
QY 372 EOLENAMVAVKTVVHGLVDFIONYSRKGHET-----POQOPNSKYTKSMCRDL 419
DB 663 VFTESRVSSQQTIVSG-----SQHEQAHSTGVFGHLPSTVQAOQSPRGVYPPSSVAOG 716
QY 420 ROQGGCPRGNTCTFAHSGOELEKYRLRNKKNATVATFPLNKVGVNNTVTAGNVISV 479
DB 717 QSOQOQ-PSSSLTGVSSSQPIQHPQ-----QQQGIQGTAPPO----- 752
QY 480 IGSTTTGKIIVSTNGISNAENSVSQILSRSTDSLRALETYKKGKGVKANCQNAQNAQPSA 539
DB 753 -----QTVQYSLSQ-TSTSSSEAT-----TAQPVSQPOA 779
QY 540 DSVTENKIGSPKPTVSNVAATSAGPSN--VGTELNSVPQKSPFLTRY-----PVYPP 591
DB 760 PQVLP-QVSAGKQLVSGQVPFTIOGEPQIPVATQSVVPHSGAHLFPVGOPLPPLP 837
QY 592 HSENIQYQDPRTQIPFEVPOY--PQTGYPPPPPTVPAGVACVPRFVRSNNVPSSSLP- 648
DB 838 -----QYVVSQIPISIPHVSTAQGTGSSLPITMAAGITQ--PLTLASSATTAATAPG 887
QY 649 -----PASMRYADHYSTSPRDRANSSPY-----QPPP-----PQYGPVPPVPSGMYAV 694
DB 888 VSTVVPSSQLP-----TLQPTVQPLPSQVHPOLLQPVQSGMGPANLQGAAYVPLSSGDVL 942
QY 695 YDSRKIMPRPMYQRDDIIRSNLSLPRMDVHSSVYQSLBERYNSLDGYVSVACQPPSEPR 754
DB 943 YOGFPRPLPQYIPGCSNLPSSSNVASCISHTVTLKPRMTEVLATPTGYPTTVQPVVSEN 1002
QY 755 TTVPL-----PREPCGHL-----KTSCEQIIRKKPDQMAQYHTQKAPLVSTLPVATQ 802
DB 1003 LTVPMGQVGGQVQVQSGSLAQAPTTSSQAVLES-----TQGVQVAPAEVAVANA 1054
QY 803 SP--TPPSPL-FSVDF-----RADSESYSGTKEEDHLSHSYPMSCGTTGSCINAI 851
DB 1055 QPQAQPTPLTASSVSAHSDVAGMSDGENENVPSSSGRHEGRTTKRHYRKSVRSRHRHK 1114
QY 852 DSEPRDVIAN-----SNAVLMDLSDQDVCRVHLFETQRTKEEDPILPFGDPIISKMG 906
DB 1115 TSPRLRLINNSNKGDRVVECOLETHNRKMTFKPDLGDNPBEIATLIVNNDPFI- 1170
QY 907 AISRSS-----RTGYHTTDPVQA-----TASQ--GSATKP 934
DB 1171 AIERESFVDQVREILEKADMLSEBVSVEBEDQGLESLQGHODYGFSGSQKLBGFQKP 1230
QY 935 ISVSDYVYVNAVDSRWSSYGNELATSSAHYVERDRFIYTDLSGHRKHS--TGDL-SL 990
DB 1231 IPASSMPOQIGIPTS-----SLTOVVAHAGR-RFIVSPVESRIRRESKVPSEBTITDV 1282
QY 991 ELQQAQKSNLLIQREANLMAQKQNSLDEGRHLTLNLISKEILRNGLQSDYEDATD 1050
DB 1283 AASTHQSPEANLSHASSLSLQOAPS-----ELRRAM-----TBGPNT 1321
QY 1051 TKPRD-----IELESLADTDEPDGSEPIEILD--IQLGISONDQ 1092
DB 1322 APNPSHGTPTFPVVPPLFSLSTAGVPTTAATAAPVPAISSPNDISTSTVIOGEVYPTRE 1381
QY 1093 LINGMAVENGAHVQOQKQEPKQKQSLGEGHVIIEBQKTIIPVTSQSPPLPVGISNNS 1152
DB 1382 GIAGVATSTGVVTSGLPIFP-----VSESPVLSVSSITIPAVVISITTS 1428
QY 1153 -CLPITTSV 1161
DB 1429 PSLQVPTTS 1438

RESULT 9
US-09-854-856-34
; Sequence 34, Application US/09854856

Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252e1 Human kinases and polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 2322
; TYPE: PR
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1) ... (2322)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-34

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QY 48 KACPDQTAINT-----DIDVLPVNFALLQVGAQVPHQSIKLSNLGEN 92
DB 315 KRASFAKSVITGPBEMABEMYEKEDSVDAFGKCHLEMATSEF----- 361
QY 93 KHYEAKKCEVEDLALYLKPLSGKGVASLNOGAL-----SRMQRKLTLYN 139
DB 362 -----YSECQNAQIYRRVTSQVK-PASPDKVAIDEVKEIIEGCIKRNKDERYSIKDLIN 415
QY 140 COLVEEGRVAMRAARSIGERTVTELLIQHNPQOLSNLMAAARACQFLGRPMQBE 199
DB 416 HAFQEEGVRVLEAEEDDEKIAIKLWRIEDIKLK-----GKYKNE 460
QY 200 AKLVIALLEDGALSARKVLVLFVVQRLERPPOAKSTSGHVQOLLYPASCFTYKRDE 259
DB 461 AIEF-----SFLERDVPBEVADQEMBSGVCEDDHTMAKATDR-- 501
QY 260 DSLMQLKEEFPSYALRRREHDAQIVHAMEAGLRI SPEQWSSLYGDLAKHSHMQSIID 319
DB 502 -VSLIKRREQR-QLVREDEQK-----KQESSLKOQVEQSSASQGIK 544
QY 320 KLQSPESPAKSVQELTIVLQRTGDP-----ANLNRLRPHLELLANIDPNDVSPW 371
DB 545 QLPASASTGIPYASTTSASVSTQVEEPEPADQHOQLQYQOQPSISVLS--DGTVDSCQGS 602
QY 372 EOLENAMVAVKTVVHGLVDFIONYSRKGHET-----POQOPNSKYTKSMCRDL 419
DB 603 VFTESRVSSQQTIVSG-----SQHEQAHSTGVFGHLPSTVQAOQSPRGVYPPSSVAOG 656
QY 420 ROQGGCPRGNTCTFAHSGOELEKYRLRNKKNATVATFPLNKVGVNNTVTAGNVISV 479
DB 657 QSOQOQ-PSSSLTGVSSSQPIQHPQ-----QQQGIQGTAPPO----- 692
QY 480 IGSTTTGKIIVSTNGISNAENSVSQILSRSTDSLRALETYKKGKGVKANCQNAQNAQPSA 539
DB 693 -----QTVQYSLSQ-TSTSSSEAT-----TAQPVSQPOA 719
QY 540 DSVTENKIGSPKPTVSNVAATSAGPSN--VGTELNSVPQKSPFLTRY-----PVYPP 591
DB 720 PQVLP-QVSAGKQLVSGQVPFTIOGEPQIPVATQSVVPHSGAHLFPVGOPLPPLP 777
QY 592 HSENIQYQDPRTQIPFEVPOY--PQTGYPPPPPTVPAGVACVPRFVRSNNVPSSSLP- 648
DB 778 -----QYVVSQIPISIPHVSTAQGTGSSLPITMAAGITQ--PLTLASSATTAATAPG 827

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QY 649 -----PASMRYADHSTSPRDMNSPY-----QPP-----PQYGPVPVPSGMYAV 694
DB 828 VSTVPSQLP-----TLQPTVQLPSQVHPQLQFVAVSGMGPANLQGAEPVPLSSGDL 882
QY 695 YDSRRIMRPMYQORDIIRNSLPPMDVHSSVYQTSLEERYNSLDGYVAVACQPPSEPR 754
DB 883 YQGFPRRLPQYRPGDSNIPSSNVASVCHSTVLXPRMTEVLATPGYPTVQPVESN 942
QY 755 TTVPL-----PREPCHL-----KTSCEBQIRRRKPDQMAOYHTQKAPLVSTLPVATQ 802
DB 943 LLVPMGVGGVQVQVSGSLAQAPTTSSQAVLES-----TQGVSQVAPAEVAVAA 994
QY 803 SP--TPPSPL-PSVDF-----RADFSESYSGTKEEDHLSHYSPMSCGTIGSCINAI 851
DB 995 QPQATOPTTLASSVDASHDVASGMSDGNENVPSSSGRHEGRTTKRHYKSVRSRHEK 1054
QY 852 DSEPKDVIAN-----SNAYLMDLSDGVKRVYHLEFQRTREEDPIPPSDGPITSKWG 906
DB 1055 TSRPKRLILNVSNKGDVAVECOLETHNRKMTVTFKFDLDGDNPEBIATIMVNDPIL----- 1110
QY 907 AISRBS-----RTGYHTTDPVQA-----TASQ-----GSATKP 934
DB 1111 ATERSEFVDQVREILEKADEMTSEDVSEVPBDOGLSLQKDDYGFSGSOKLEGEFKOP 1170
QY 935 ISVSDYVPVYNAVDSRWSYSGNEATSSAHYVERDFIVTDLSGHRGSS--TGDLL-SL 990
DB 1171 IPASSMPQOIGIPTS-----SLTQVHVSAGR-RITVPSPESSRLRESKVPSEITDIV 1222
QY 991 ELQAKSNLLLOREANALAMQOKNSLDEGRHLTLNLKSELLENGLQSDYTEADAT 1050
DB 1223 AASTQSPGMNLSHSASLSLQDAFS-----ELRRQM-----TEGPNT 1261
QY 1051 TMPDD-----IELESLADTDEPDGSEPIEILD--IOLGISSONDO 1092
DB 1262 APPNSHTPTTPVVPPELSSLAGVPTTAATPVPATSPPDISTSYIQSVYPTPE 1321
QY 1093 LINGMAVENGHVPOHQEPKOKSLGEDHVILEQKTIIPVTSFSGPLPVSISSNS 1152
DB 1322 GIAGVATVSGVATSGGLPIPP-----VESPVLSVSVSITIPAVVISITTS 1368
QY 1153 -CLPITTSVS 1161
DB 1369 PSLQVPTSTS 1378

RESULT 10
US-10-010-720-34
; Sequence 34, Application US/10010720
; Patent No. 6858419
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Made
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hansen, Gwenn
; APPLICANT: BeltrandelRio, Hector
; APPLICANT: Van Slichtehorst, Isaac
; TITLE OF INVENTION: No. 6858419el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same, And Uses Thereof
; FILE REFERENCE: Lex-0382-USA
; CURRENT APPLICATION NUMBER: US/10/010/720
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/854,856
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 2322
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

```

```

; NAME/KEY: VARIANT
; LOCATION: (1)....(2322)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-010-720-34

Query Match      3.1%; Score 194; DB 2; Length 2322;
Best Local Similarity 18.5%; Pred. No. 1.1e-05;
Matches 235; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

QY 48 KACPFDQTAINT-----DIDVFPVNFALLQLVGAQVPHQSIKLSNLGEN 92
DB 315 KRASPAKSVTIGTPEPMABPMTEEKYDESVDYAFKCHLBMATSEYP----- 361
QY 93 KHVEYAKKVEDLALYLKPLSGKGVAISLQSL-----SNPMQRKVLTVN 139
DB 362 -----YSECQNAQOYRRRTSGVK--PASFDKVALEVEKIEIGCIRONDERYSTKIDLN 415
QY 140 COLVEBGRVAMRAARSLGERTTTELLIQHONPOOLSANLMAAVRAGCQVLGRPMQBE 199
DB 416 HAFQEBETGVVELAEEDGEXIAIKLWLIEDIKLK-----GKYKNE 460
QY 200 ALKVLVLLLEDGSAISRKVLVFPVQRLERRPPQASKTSIGHVOLLVYRASCFTKTRDE 259
DB 461 AIEP-----SFLERDVPEDVQABMYESGYVCEGDHKTAKAIKDR-- 501
QY 260 DSLNQLKEEPRSYEARREHDAQIVHIAEAGLRISPQWSSLVYGLAHKSHMQSIID 319
DB 502 -VSLIKRREGR--QVREGEKK-----KQESSLKQVEQSSASQGTGX 544
QY 320 KIQSPBSFAKSVQELTYLQRTGDP-----ANILRLRPLELLANIDPNDVASPTW 371
DB 545 QLPASATGIPATSTTASVSTOVEBERPADHQOLQVQFPISYLS--DGTVDGQGS 602
QY 372 EQLENAMVAVKTVHGLVDFIQNYSRKGHET-----POPQPSKYTKSMCRDL 419
DB 603 VTTESKVSQQTAVSG-----SCHQASHSTGVCHISTVQAQSQPHGYTPPSSVAG 656
QY 420 ROQCGPRGTNCTFASQBLEKYRLRNKNATVATPPLNKVGVNNTVTTAGNVISV 479
DB 657 QSQGQ--PSSSSLTGVSSSQPIQHPQ-----QQQGIQGTAPQ----- 692
QY 480 IGSTETTKIVPSTNGISNAENSVSQILSRSTDSITRALETYKVKVQVANGQNAAGPSA 539
DB 693 -----QTVQYLSQ--TSTSEAT-----TAQVPSQPA 719
QY 540 DSVTENKIGSPKTPSVNVAATSAGPSN--VGTSLNSVPQKSPFLTRY-----PVYPP 591
DB 720 PVLPR-QVASAGKQLPVSPVPTIQEPQIPVATQPSVNVHSGANLPGQPLPTLLP- 777
QY 592 HSENIQFQDPRTOIPFEVPOY--PQTGYPPPTVPAGVAPCVPRFVSNVPESSLP- 648
DB 778 -----QYVSQLPISITPHVSTAGTGSPLITMAAGITQ--PLTLASSATTAIRG 827
QY 649 -----PASMRYADHSTSPRDMNSPY-----QPP-----PQYGPVPVPSGMYAV 694
DB 828 VSTVPSQLP-----TLQPTVQLPSQVHPQLQFVAVSGMGPANLQGAEPVPLSSGDL 882
QY 695 YDSRRIMRPMYQORDIIRNSLPPMDVHSSVYQTSLEERYNSLDGYVAVACQPPSEPR 754
DB 883 YQGFPRRLPQYRPGDSNIPSSNVASVCHSTVLXPRMTEVLATPGYPTVQPVESN 942
QY 755 TTVPL-----PREPCHL-----KTSCEBQIRRRKPDQMAOYHTQKAPLVSTLPVATQ 802
DB 943 LLVPMGVGGVQVQVSGSLAQAPTTSSQAVLES-----TQGVSQVAPAEVAVAA 994
QY 803 SP--TPPSPL-PSVDF-----RADFSESYSGTKEEDHLSHYSPMSCGTIGSCINAI 851
DB 995 QPQATOPTTLASSVDASHDVASGMSDGNENVPSSSGRHEGRTTKRHYKSVRSRHEK 1054
QY 852 DSEPKDVIAN-----SNAYLMDLSDGVKRVYHLEFQRTREEDPIPPSDGPITSKWG 906
DB 1055 TSRPKRLILNVSNKGDVAVECOLETHNRKMTVTFKFDLDGDNPEBIATIMVNDPIL----- 1110

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Qy 907 AISRSS-----RTGVHTTDPVQA-----TASQ---GSATKP 934
Db 1111 AIERESFVDQVEIIEKADENLSEDEVSPBEDQGLSEIQGKDDYGFSSQKLBGEFFKOP 1170
Qy 935 ISVSDYVPVNAVNDRWSSYGNENATSSAHYVERDRFIYVTLDSGHRKHS---TGDLL-SL 990
Db 1171 IPASSMPOQIGIPTS-----SLTQVYHSAQR-RFIVSPVESRLREKVPSEITDVI 1222
Qy 991 ELQQAQKSNLLIQREANALAMQOKKNSLDEGRHLLTNLSKEIELRNGELQSDYEDATD 1050
Db 1223 AASTAQSGMNLSSHASSLSIQQAFS-----ELRRQM---TEGPNT 1261
Qy 1051 TKPRDD-----IELESLDTPDEPDGQSEPIEILD---IOLGISQNDQ 1092
Db 1262 APPNFSHGPTFPVVPPLSSIAGVPTTAATAVPATSSPPNDISTSVIQSEVPTPEE 1321
Qy 1093 LLNGAVENGHPVQOQKPPKOKQSLGEBHVILEEQKTLIPVTSQSFQPLPVASISNAS 1152
Db 1322 GIAGVATSTGVVTSGLPIPP-----VSESPLVSSVSSITIPAVVISISTTS 1368
Qy 1153 -CLPITTSVS 1161
Db 1369 PSLQVPTSTS 1378

RESULT 11
US-09-854-856-2
; Sequence 2, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854, 856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206, 015
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2382
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2382)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-2

Query Match 3.1%; Score 194; DB 2; Length 2382;
Best Local Similarity 18.5%; Pred. No. 1.2e-05;
Matches 235; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

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Qy 260 DSSLMLQKEEPPSYEARLREHDAQIVHTAMEAGLRISPEQWSSLYGDLAKHSHMOIID 319
Db 562 -VSLIKRREQR--OLVBEQEK-----KQESSLKQOYEQSSASSTGK 604
Qy 330 KLOSPESPAKSVQELTIVLQRTGP-----ANLNLRLPHLELLANIDPNDAVSPTW 371
Db 605 QLPASASTGIPSTASTSASVSTQVEBEADQHQOQYQQFISVLS--DGVTSQGGSS 662
Qy 372 EOLENAMAIVKTVHGLVDFIQNYSRKHET-----PQDPMSKKTSMCRDL 419
Db 663 VTEBSRVSSQQTVSYG-----SOHEQASTGTGVGHIPSTVQAQSQPGHVPSPSSVAQ 716
Qy 420 RQGGCPRGNTCTPAHSQEELEKYLRLNKKINATVTRPFLNKLKVGNNVTTAGNVISV 479
Db 717 QSQGO-PSSSSLTGVSSSOPQIHPQ-----QQGIGQOTAPPO----- 752
Qy 480 IGSTETTGKIYPTNGISNAENSVSQLSKSTDTSLRALETYKVKVKGANGQANAPSA 539
Db 753 -----QTVQYSLSQ-ISTSEAT-----TAQPVSQQA 779
Qy 540 DSVTENKIGSPKPTVSNVATSSAGPSN--VGTELNSVPQKSSPLITRY-----PVPP 591
Db 780 PQVLP-QVSAGKQLPVSQGPVPTIGEPQIPVATOPSPVPHSGAHFLPVQGPLPTPLP- 837
Qy 592 HSENIQYQDPRTOIPEFVPOY--PQTGYPPPTVPAGVACVPRFVSNVPESSLP- 648
Db 838 -----QYVQSQIPSTPHVSTAGTQGSPLPTMAAGITO--PLVTLASSATTATIG 887
Qy 649 -----PAMPYADHSTSPDRMNSPY-----QPP-----POPYGPVPVPPSGYAV 694
Db 888 VSTVPSQLP-----TLQPTVQLPSQVHPQLQAVQSGMIPANIGQAQAEVPLSGDVL 942
Qy 695 YDSRRIIMPYQKQDDIIRNSLPRMDVHSSVYOTSLERKNSLDGYVSAVCQPPSEER 754
Db 943 YQGFPPRLPQYQGSNIAFSSNSVAVCHSVTLKPPMTEVLATPGVFPVTVQPVESN 1002
Qy 755 TTVPL-----PREPGHL-----KTSCEBDIRKKPDQMAUHQKAPLVSTLPVATQ 802
Db 1003 LLVPMGVGVGOVQVQPGGSLAQAPTSSQAVLES-----TQVSVQVPAEVAVA 1054
Qy 803 SP--TPSPPL-FSYVP-----RADPSESVGTKFEEDHLSHSPMSCGTIGSCINA 851
Db 1055 QPQATQPTLLASSVDSASDVASGMSDGNBNVPSSSGRHEGRTTKRHYKSVRSRHRBK 1114
Qy 852 DSEPKDVIAN-----SNAYLMDLDSGVYKRVHLETQRTKEEDPPIFSPGPIISKMG 906
Db 1115 TSPRLRILNNSNKGDRVVECOLETHNRKMVTFKFDLDGDNPEBIATIMVNDPILV---- 1170
Qy 907 AISRSS-----RTGVHTTDPVQA-----TASQ---GSATKP 934
Db 1171 AIERESFVDQVEIIEKADENLSEDEVSPBEDQGLSEIQGKDDYGFSSQKLBGEFFKOP 1230
Qy 935 ISVSDYVPVNAVNDRWSSYGNENATSSAHYVERDRFIYVTLDSGHRKHS---TGDLL-SL 990
Db 1231 IPASSMPOQIGIPTS-----SLTQVYHSAQR-RFIVSPVESRLREKVPSEITDVI 1282
Qy 991 ELQQAQKSNLLIQREANALAMQOKKNSLDEGRHLLTNLSKEIELRNGELQSDYEDATD 1050
Db 1283 AASTAQSGMNLSSHASSLSIQQAFS-----ELRRQM---TEGPNT 1321
Qy 1051 TKPRDD-----IELESLDTPDEPDGQSEPIEILD---IOLGISQNDQ 1092
Db 1322 APPNFSHGPTFPVVPPLSSIAGVPTTAATAVPATSSPPNDISTSVIQSEVPTPEE 1381
Qy 1093 LLNGAVENGHPVQOQKPPKOKQSLGEBHVILEEQKTLIPVTSQSFQPLPVASISNAS 1152
Db 1382 GIAGVATSTGVVTSGLPIPP-----VSESPLVSSVSSITIPAVVISISTTS 1428
Qy 1153 -CLPITTSVS 1161
Db 1429 PSLQVPTSTS 1438

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RESULT 12
US-10-010-720-2
; Sequence 2, Application us/10010720
; Patent No. 6858419
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hansen, Glenn
; APPLICANT: BeltrandelRio, Hector
; APPLICANT: Van Sligtenhorst, Isaac
; TITLE OF INVENTION: No. 6858419el Human Kinases and Polynucleotides
; FILE REFERENCE: LEX-0382-USA
; CURRENT APPLICATION NUMBER: US/10/010,720
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/854,856
; PRIOR FILING DATE: 2000-05-14
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2382
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2382)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-010-720-2

Query Match      3.1%; Score 194; DB 2; Length 2382;
Beet Local Similarity 18.5%; Pred. No. 1,2e-05;
Matches 235; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

48 KACPEDQTAINT-----DIDVLPVNFALLQVGAQVDPDHQSIKLSNLGEN 92
375 KRASFSAKSIIGTPEFAPMEYBEKYDESVDVYAFGCMLEMATSEPR----- 421
93 KRIYVAKKQVEDLALYLKPLSGGKGVASLNOSAL-----SRPMOKVLTVN 139
422 -----YSECQNAAQIRRYRTSGVK-PASFPKVAIPVKEIIIEGCIKQNDERSISIDLIN 475
140 COLVEEGRVARMARSLGERTVELLIQHONPQOLSANLMAAVARAGCQFLGRAMQE 199
476 HAPFOETGVVLEEDDEKIAIKMLRIEDIKLK-----GKYKNE 520
200 ALKLVLLALEDGSALSRKVLVLFVVQRLPFRPQASKTSGHVVQLLYRASCCKVTKRDE 259
521 AIEF-----SEDLERDVPEDVAQEMVSGYVCEBDHTMAKAIKDR-- 561
260 DSSLMOQLKEEFSEYELAREHDAQIVHIAEAGLRISPEWSSLLYGLLAHSHMOSIID 319
562 -VSLIKRKEQR--QLVREEQEK-----KQESSSLKQVQEGSASQTGIK 604
320 KQSPSPFAKSVQELTIVQRTGDP-----ANLNRLRPHIELLNDPNDAVSPW 371
605 QLPASASTGIPJASTTSASVSTQVEEPEDADHQLOQOQPSISVLS--DGTVDSSQSS 662
372 EOLENMAVVKTVVHGLVDFIQNSRKGHET-----PQPPNSKYTKSKRDL 419
663 VTESVSSQOQIVSYG-----SQHQASHTGIVPHGISVTVQAQSQPHGVPPSSVAG 716
420 ROQGGCPRGNTCTFAHSGELEKXYRLRNKKINATVTFPLLNKVGVNNTVTAGNVISV 479
717 QSGQGQ-PSSSSLGVSSQPIQHPQ-----QQQGIQGTAPPO----- 752
480 IGSSTTGKIVPTNIGSNAENSVQILSRSTDSLTALETVKKVKGANQNGNAGPSA 539
753 -----QTVQVYLSQ-TSTSEAT-----TAQVPVQPOA 779

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540 DSVTENKIGSPKPEVSNVAATSAGPSN--VETELNSVPQKSSPFLTRV-----PVYPP 591
780 PQVLP-QVSAGKQLVPSQVPFTIGEPQIPVATGSPVVPVSHGAFHLPVGCPLPFLP- 837
592 HSENIQYFODRPTQIPFEVPOY--PQTGYPPRPVTPVAGVACVRFRRSNVPPSSLP- 648
838 -----QYVPSQIPSTPHVSTAGTGFSSLPITMAAGITQ--PLTLASSATTAALPG 887
649 -----PAMPYADHSTFSPDRMNSPY-----QPP-----POPYGPVPVPSGMYAV 694
888 VSTVPSQLP-----TLQPYQLPSQVHPQLQAVQSMGIPALQGAELPSSGDL 942
695 YDSRRIMRPYXORDIIRNSLPRMDVHSSVQTSLRERYNSLDGYVAVACQPPSEPR 754
943 YCGFPRRLPQYVPGDSNIAPSNSVASCISHSVLXPRMPEVTLANPGYFPVYQYVESN 1002
755 TTVPL-----PREPCGHL---KTGCEBQIRRKPRDQMAQYHQAQVLSSTLPVATQ 802
1003 LLVPMGVGQGVQVQSPGGSILAQAPRTSSQAVLS-----TQVSGVAPAEVAV 1054
803 SP--TPPSPL-PSVDF-----RADFSESVGTGFEDHLSHPMSCGTIGSCINAI 851
1055 QPQATQPTTLASSVDASDVASGMSDGENVPSSSGRHEGTTGRHRYKSVRSRHEK 1114
852 DSEPRDVIAN-----SNAVLMDSGDVYKRVHLFETQRTYEEDPIIPSDGPIISKMG 906
1115 TSRPKLRILNVGNKGDVVECOLFETHNRKMTVFKEFDLDGNDPELATIMVNNDFIL- 1170
907 AISRSS-----RTGYHTTDPVQA-----TSQ---GSATPK 934
1171 ATERSSFVDQVREIIEKADEMISEDVSVPEBDQLESIQGDDVDFSGSQLEGFQKP 1230
935 ISVDYVPYVNAVDSRWMSYGNEDATSAHYVERDRFIYTDLSGHRKHS--TGDL--SL 990
1231 IYASSMPQOIGIPTS-----SLTQVHSAQR--RFVSPVESLURESKVPSEITDQV 1282
991 ELQAKSNLSLLQREANALAMQOKNNSLDEGRHLLTNLSKEIELRNGSLQSDYEDATD 1050
1283 AASTAQSPQMNLSHASSLSLQAFS-----ELRRQM---TEGPYT 1321
1051 TKPRPD-----IELESLDTPDEPDQOSEPIEILD--IQGISGQNDQ 1092
1322 ADPNFSHTGPTFPVVPFLISSIAGVPTTAATAVPVPAISSPNDISTSYIOSEVYPTBE 1381
1093 LINGMAVENGHVPVQHQKEPPKQKQSLGEDHVLIEBQKTLIPVTSQFQPLPVSISSNAS 1152
1382 GIAGVATSGVVTSGGLPIPP-----VSESPVLSVSSITTPAVVISITTS 1428
1153 -CLPITTSVS 1161
1429 PSLQVPTSTS 1438

RESULT 13
US-09-854-856-48
; Sequence 48, Application us/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 1939

```

```

; TYPE: PRt
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)....(1939)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-48

Query Match      3.1%; Score 193.5; DB 2; Length 1939;
Best Local Similarity 19.2%; Pred. No. 9e-06;
Matches 256; Conservative 168; Mismatches 527; Indels 379; Gaps 57;

QY 114 GKGVAASINQSLSPRMOKLVTIVNCOVLEEGRVR-AMRAARSLGERTVELLIQHON 172
DB 660 GQSSSSSLTGVSSQPIQHPOOQOGIQOTAPPOQTVQVSLSTSTSSSEATTAQVPSQPOA 719
QY 173 POOLSANLMAAVRANGCOFLGPA-----NOEALKLVLALDEGALSRRKVLVLFVQRL 227
DB 720 PQVLPQVSAGKSTGQSVQVAPAEPAVAVAQPOATQPTTLASSVDSAHSD---VASGMSDG 776
QY 228 EERFPOASTISIGHVQVLLYRASCFKVTYKREDSCIMQK-----EERFSTYALRRED 281
DB 777 NENVSSSGRHHGRITTKRHYRKS-VSRSRHKEKTSRPKLRIINVSNGKGRVVECOLETHN 835
QY 282 AQIVHIAWAGARISPEQWSSILY-GDLAKHSMQSIIDKQSPSEFAKSVQELTIVLQR 340
DB 836 RKMVTFKFDLD-GDNREELATIMVNDPILALIERSEFVDQVREILIEKADEMPLSEDSVVR 894
QY 341 TGDPAINLRLRPHLELLANID-----PNPDVSPTEQLLENAMVAVKTV 384
DB 895 EGDQG-----LESLOGKDDYGFSGQKLEGFEKQPIIPASSMP--QCIIGIPITSLLQV 944
QY 385 VHGLVDFIOWYRKRKHETPOPOP-----SKYTSKCRDLRQCGCPRGCTNCTFAHS 436
DB 945 VH-----SAGRRTFVSPVESRLSESKVFPSEIDTVAASGASPG-----NMLSHS 991
QY 437 QELEKVR---LRMKI-----NATVTRTP-----LKNVGNNTVTJTA--- 473
DB 992 ASLSLQQAQFSELRRQMTGEPNTAPPNFSHTGPTFPVPPPLSLASGAVPTTAAAPVP 1051
QY 474 -----GNVIVIGSTETGKIVPSTNGISNAENS-----VSQLS 508
DB 1052 ATSSPNDISTSVISQEV---VPTEEGIAVASTGVTSGGLPIPIPVSESPVLSVVS 1108
QY 509 RSTDTLRALETVKYKVGKVGAN-----GQNAAGPSAD-SYENKIG---SPKTPVSN 557
DB 1109 SITIPAVVSIITSPSLQVPTSTSEIVSSTALYPSTVATSASAGSGSTATPGKPAVP 1168
QY 558 VAATSAGPSNVGTETNSV-----PQSSPFLTRVPVYPHSENIOYF 599
DB 1169 VSQAAGSTTVGATLTSVTTTSPBSTASQLSIQSSSTSTPTLAEVVVAASHLD-KTS 1227
QY 600 QDPRTQIPEVPOVQOTGYRPPPP-----TVAGVAPCV-PRFVSNVNPBESSLPASMP 653
DB 1228 HSTTGLAFSL-SAPSSSSSPGAGVSYISQPGGLHPLVIPSIAVSTPLLPQAAGTSTFP 1286
QY 654 YADHSTSPDRKMSPPYQPPPPQYGFVPVPSGM-----YAPVDS 697
DB 1287 L-----LPQVPSIPPLVQPVANVPVVOQTILHSQPOPALLPMPHTHCPEVDS 1334
QY 698 RRIWRPMWQRDDI-----IRS--NSLPRMDVMSV-YQTSLRERNVSLDGYVVA-- 746
DB 1335 DT--QPKAPGIDIDITLKEKLSLSESHSSGAQHASVSLSTVLESTVTGPIPTTAA 1392
QY 747 -----CQPSSE-PRITVPLPREBC--GHLKTSCEEQIIR-KPDQMAQYHTQKA 790
DB 1393 PEKLLSTSTSLCPINPLGLVIALPVTVTPGQVSTVSTTSSVTKGT-----APSKP 1448
QY 791 PLVSS- TLPAVATQSPPPSPLFSVDFRADFSSESVSSTKFEEDHLSHYSWSCGTIGSCIN 849
DB 1449 PLTKRPAVLPVGTGLP-----AGTLPS--E 1470
QY 850 AIDSEPKDVITANSNMVIMDLS-----GDVGRVHPLPETQRRK----- 888

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DB 1471 QLPFFGSLTNSQOPLLEDLDQLRRTLSPEXITVTSANGVPSMAAPTAITAGTQPOKG 1530
QY 889 ----EEDPIIPSPDPIISKWG-----AISRSSRTGHTTDPVATASQSATKPIVS 938
DB 1531 VSQVKEGPVLTATSGAGVFKMGKRPQVSVAAQAKQEGKKKSBDKSVHFESESTESSVLS 1590
QY 939 DYVPYVNAV-----DSRMSYGNENAS-SAHYVERDRFITYDLS---G 977
DB 1591 SSSPSTLVKPPPNIGITIPGSSDVPESAHKTTTASBKSDTQPTKVGRFQVTTANKVG 1650
QY 978 HRKHSSTGDLSS-----LELOQAKSNLILLOREANALAMQKMN----- 1016
DB 1651 RFSVSKTEBDKTDITKKEGVASPPMDLEQAVLPVPIPKKEKPELSEPHLNGPSSDPPA 1710
QY 1017 ----SLDEGR--H-TNLNLSKEIELRN-----GELQSDY-TEDATDKPRDRIELE 1061
DB 1711 AFLSRDVEDGSGSPHQSLSKSLPSQVLSQSLSNSFNSSYMSDNESEDIDEDIKLEL 1770
QY 1062 SALDDEPDQSEPIEILIDQLGISSONDQLN-----GMAVENGHPRVQHOKEPRK 1114
DB 1771 RRL-----RDKHLKEIQDLSRQKHETESLYTKGVPPAVIIPPAAPLSGRRRPTK 1823
QY 1115 OK-----KQSLGEBH-----VILEQKTLIPVTSQFSGQPLVPSISNACLP 1155
DB 1824 SKGSKSSRSSSLGKNSPOLSGNLSCQSAASVLIHPQOTLHPGN-----IPESQONLLQP 1878
QY 1156 ITTSVAGNL 1165
DB 1879 LKPSPSDNL 1888

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RESULT 14
US-10-010-720-48
; Sequence 48, Application US/10010720
; Patent No. 6858419
; GENERAL INFORMATION:
; APPLICANT: walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hansen, Gwenn
; APPLICANT: BeltrandelRio, Hector
; APPLICANT: Van Sligtenhorst, Isaac
; TITLE OF INVENTION: No. 6858419el Human Kinases and Polynucleotides
; FILE REFERENCE: Encoding the Same, And Uses Thereof
; CURRENT FILING DATE: 2002-05-21
; CURRENT APPLICATION NUMBER: US/10/010,720
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/854,856
; PRIOR FILING DATE: 2000-05-14
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 1939
; TYPE: PRt
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)....(1939)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-010-720-48

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Query Match      3.1%; Score 193.5; DB 2; Length 1939;
Best Local Similarity 19.2%; Pred. No. 9e-06;
Matches 256; Conservative 168; Mismatches 527; Indels 379; Gaps 57;

QY 114 GKGVAASINQSLSPRMOKLVTIVNCOVLEEGRVR-AMRAARSLGERTVELLIQHON 172
DB 660 GQSSSSSLTGVSSQPIQHPOOQOGIQOTAPPOQTVQVSLSTSTSSSEATTAQVPSQPOA 719

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QY 173 POOLSANLMAVRAGCQFLGPA-----MOEALKVLVLLALBDGSLRSKVLVLFVVOQL 227
DB 720 POVLPOVSAKOSTGVSGVAPAEPAVAQAPOATOPTTLASSVDSAHSD---VASGMSDG 776
QY 228 EPRFPOAKSTISGHVVOLLYRASCFKVTKRDESSIMQK-----EPRSYEALREHD 281
DB 777 NENVSSSGRHEGRTTKRHYSKS-VRSRREKTSRPKRLINLVNSKGRVVECOLETHN 835
QY 282 AOIYHIAEAGLRISPEOMSSLLY-GDLAKHSMOSIIDKLOSPESFAKSVQELTIVLOR 340
DB 836 RKMVTFKFDLD-GDNPEBIATIMVNNDFILALERSFVDQVREIIEKADMLSEDEVSRP 894
QY 341 TGDPANLRLRPHLELANID-----PNPDVSPTEQLENAVAVKTV 384
DB 895 EGDGQ-----LSLQCKDDYGFSGSKLEGEFKQPIPASMP--QOIGIPTSLLTOY 944
QY 385 VHGLVDFIOWYARKHETPOPOP-----SKYKTSKCRDLROQCGCPRGNTCTFAHS 436
DB 945 VH-----SAGRRFIVSVPRSLRESKVPFSEITDVAASTAQSPG-----NMLSHS 991
QY 437 OBELEKYR-----LRNKKI-----NATVRTPP-----LNLKVGNNTVTTTA--- 473
DB 992 ASLSLQAFSELRAQMTGPNTPAPNFSHTGPTFPVVPPLSLIAGVPTTAATAVPV 1051
QY 474 -----GNVISVIGSTETTKIIVPSTNGISNAENS-----VSOLIS 508
DB 1052 ATSSPNDISTVIOSEVT---VPTBEGIAGVATSTGVTSGLPIPVSESPVLSSVVS 1108
QY 509 RSTDSTLRALETVKVKYKVGAN-----GQNAAGPAD-SVTENKIG---SPKTPVSN 557
DB 1109 SITIPAVVASITSPSLQVPTSTSEIVASTALYPVSATASAGSGSTATPGKXPAY 1168
QY 558 VAATAGBNVCTELNSV-----POKSSPFLRVVPYPPHSENIQVF 599
DB 1169 VSQQAAGSTTVGATLTSTVSTTSPBSTAQLSIQLSSSTSTPLAETVVVAASHLD-KTS 1227
QY 600 QDPRTQIPEVPEQYQOTGYPPPP-----TVPAGVAPCV-PFVVASNNVPESLLPPASMP 653
DB 1228 HSSTTGIAFSL-SABSSSSSPAGVASYISQOGLHPLVIPSVIASTPLLPQAGTSTFP 1286
QY 654 YADHYSTSPRDRMNSPPQPPPOPYGPPVPSGM-----YAVVDYS 697
DB 1287 L-----LPQVPSIPLVQPVANVPAVOQLHSQPOPALLPNOPTHCEVDVS 1334
QY 698 RRTMPPMYQORDI-----IRS-NSLPRMDVMHSSV-YQSLARKVNSLDGYVVA--- 746
DB 1335 DT--QPKAGDIDIKTLEKRLSLPSEHSSSGAQHASVLETSLVIESVTVPRTTAVA 1392
QY 747 -----COPSE-PRITVPLPREPC---GHUKTSCBEQIRK-KPDQMAOYHTQKA 790
DB 1393 PSLKLTSTTSTCLPRTNPLGLTVALPVTVPVPGQVSTVSTTSGVKGT---APSKP 1448
QY 791 PLVSS-TLPVATQSPTPSPPLFSVDFRADPSBSVSGTKEEDHLSHYSPWSCGTIGSCIN 849
DB 1449 PLTKAPVLPGTELP-----AGTLPS--E 1470
QY 850 ALDSEKQVIANSNVIMLMDLS-----GDVRYRHLFETQARK- 888
DB 1471 QLPPEPGPSLTOSQOPLDLDLQALRRTTSLPEKITVTSAGVPVMAAFTAITTEGTPOKA 1530
QY 889 -----EEDPITPFSDGPIISKWG-----AISRSSRTGYHTDPVQATASQSAKTPISVS 938
DB 1531 VSQVKEGPLATSSGAGVFKMGRFOYSVAADGAQKSKSBDKSVHFESSSTSESVSLS 1590
QY 939 DVVPYVNAV-----DSRWSSYGNBATS-SAHYERDRPIVTDLS--G 977
DB 1591 SSSPSTLVKPEPNGITITPGISDVDESAAKTTASBAKSDTQOPTKVGFOVTTANKVG 1650
QY 978 HKKHSSTGULLS-----LELOAKSNSLLQREANALMOQKN----- 1016
DB 1651 RFSVSTTEKTIKTJKEGPVAPSPFMDLQOAVLPAVTPKKEKPELSEPHLNPSSDDPEA 1710
QY 1017 -----SLDEGR--HLLMLNLKREILRN-----GELQSDY-TEDATDTKPPDRIDLEL 1061

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DB 1711 AFLSRDVEDGGSGSPHSRPHQLSKSLPSONLBSQSLNSFNSSVMSDMSJEDDEDLKLLEL 1770
QY 1062 SALDTDEPDGQSEPTPEELIDTQLGISSQNDOLN-----GMAVENGHVPVQHOKEPPK 1114
DB 1771 RRL-----RDKHKEIIDLQSRQKHEIESLYTKGVPPAVITIPPAAPLSGRRRRTPK 1823
QY 1115 OK-----KOSIGEDH-----VILEQKTLIPVTSFSPQPLVVISNASCLEP 1155
DB 1824 SKGSSSSSSSSSGKSPOLSGNLGSGSAASVHLPOQTLHPRON-----IPESGQVQLQF 1878
QY 1156 ITTSVSAQNL 1165
DB 1879 LKPSPPSNDL 1888

RESULT 15
US-09-854-856-16
; Sequence 16, Application US/0984856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hildun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1999
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1999)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-16

Query Match 3.1%; Score 193.5; DB 2; Length 1999;
Best Local Similarity 19.2%; Pred. No. P.5e-06;
Matches 256; Conservative 168; Mismatches 527; Indels 379; Gaps 57;

QY 114 GSKGVASLQNSALSRPMQKVLTVNCOIVEEGRVR-AMRAARSLGERTVTELLIOHON 172
DB 720 GQPSSSLTGVSSQPIQHPOQOQGIQOTAPPOQTVQVLSQSTSSSEATTQAQVSOQPA 779
QY 173 POOLSANLMAVRAGCQFLGPA-----MOEALKVLVLLALBDGSLRSKVLVLFVVOQL 227
DB 780 POVLPOVSAKOSTGVSGVAPAEPAVAQAPOATOPTTLASSVDSAHSD---VASGMSDG 836
QY 228 EPRFPOAKSTISGHVVOLLYRASCFKVTKRDESSIMQK-----EPRSYEALREHD 281
DB 837 NENVSSSGRHEGRTTKRHYSKS-VRSRREKTSRPKRLINLVNSKGRVVECOLETHN 895
QY 282 AOIYHIAEAGLRISPEOMSSLLY-GDLAKHSMOSIIDKLOSPESFAKSVQELTIVLOR 340
DB 896 RKMVTFKFDLD-GDNPEBIATIMVNNDFILALERSFVDQVREIIEKADMLSEDEVSRP 954
QY 341 TGDPANLRLRPHLELANID-----PNPDVSPTEQLENAVAVKTV 384
DB 955 EBDGQ-----LSLQCKDDYGFSGSKLEGEFKQPIPASMP--QOIGIPTSLLTOY 1004
QY 385 VHGLVDFIOWYARKHETPOPOP-----SKYKTSKCRDLROQCGCPRGNTCTFAHS 436
DB 1005 VH-----SAGRRFIVSVPRSLRESKVPFSEITDVAASTAQSPG-----NMLSHS 1051
QY 437 OBELEKYR-----LRNKKI-----NATVRTPP-----LNLKVGNNTVTTTA--- 473

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Db 1052 ASSLIOQA FSELRAQMTGENTAPBNSHTGPTFPVPVPPFLSSAGVPTTAATAVPV 1111
QY 474 -----GNVISVIGSTETTGKI VPTNGISNENS-----VSQJIS 508
Db 1112 ATSSPNDISTSVIOSEVT---VPTBEGIAGVATSGVTLGPPIPVSESPVLSSVVS 1168
QY 509 RSTDSTLRALETVKVKYKGAN-----QONAGPSAD-SVTENKIG----SPPKTPVSN 557
Db 1169 SITIPAVVISITSSPSLOVPTSTSEIVSSALYPSVTVSATSASAGSTATPGPKPVAV 1228
QY 558 VAATSAGSPSNVGTENSV-----POKSPFLTRVPVYPPHSENIQYF 599
Db 1229 VSQQAAGSTTVGATLTSTVSTTSFPTASQLSIQSSSTSTPTLAETVVVSAHSLD-KTS 1287
QY 600 QDPRTQIPEEVPOYQOTGYPPPP-----TVPAVAPCV-PREVSNVNPBESSLPASMP 653
Db 1288 HSTTGIAFSL-SAPSSSSPGAGVSSYISQPGIHLPLVTPSVIASTPILPQAAGPTSTP 1346
QY 654 YADHSTSPRDRMNSPYQPPPPGYGVPPVPSGM-----YAPVYDS 697
Db 1347 L-----LPQVPSIPPLVQPVANVPAVOOTLIHSQOPALLPNQPTHCEVYDS 1394
QY 698 RRIWRPMYQRDDI-----IRS--NSLPRMDVMHSSV-YOTSLRERNVSLDGYSSVA-- 746
Db 1395 DT--QPKAPGIDITLBEKLRSLSEHSSGAQHASVSLTSLVIESTVTPGIPTTAVA 1452
QY 747 -----CQPPSE-PRITVPLPREBC--GHLKTSCEEOIRR-KPDQWAQYHTOKA 790
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QY 850 AIDSEPKVIANSNVIMDLDS-----GDVGRVHLFEQRTK---- 888
Db 1531 QLPPEGSELTOGQPLEDLDAQLRRTLSPEXITVTSAVGPVSMAPTAITEAGTOPQKG 1590
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QY 1017 -----SLDEGR---HLTNLILSKEIERN-----GELQSDY-TEDATDTKPPRDIETEL 1061
Db 1771 AFLSRDVDDGSGSPHSPLQLSKSLPSCQLSGLSLNSFNSSYMSSDNESDIEDDKLEL 1830
QY 1062 SALDTDEPDGQSEPIEILIDILGJISSQNDOLN-----GMAVENGHVQOHQKEPPK 1114
Db 1831 RRL-----RDKHKEIQDLOSROKHEIESLYTKLGKVPVAVIIPPAAPLGRRRRPYK 1883
QY 1115 OK-----KQSLGEBH-----VILEBOKTILPVTSCTFSQPLPVISNASCPL 1155
Db 1884 SKGSYKSSRSSSLGNKSPOLSGNLGSGQSAASVILHPQOTLHPGN-----IPESQONOLLOP 1938
QY 1156 ITTSVSAGNL 1165
Db 1939 LKPSPSDNL 1948

Search completed: May 24, 2006, 12:49:35
Job time : 37 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 24, 2006, 12:51:25 ; Search time 112 Seconds
(without alignments)
4925.794 Million cell updates/sec

Title: US-10-619-992-2

Perfect score: 6215
Sequence: 1 MPVQAQWTEFLSCPTCYNE.....MSEKNDFLKPVANGKMNVS 1191

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6215	100.0	1191	3	US-09-921-099-2 Sequence 2, Appl1
2	6215	100.0	1191	5	US-10-619-992-2 Sequence 2, Appl1
3	6207	99.9	1191	3	US-09-921-099-4 Sequence 4, Appl1
4	6207	99.9	1191	5	US-10-619-992-4 Sequence 4, Appl1
5	5483	88.2	1048	5	US-10-619-992-8 Sequence 8, Appl1
6	1538	24.7	819	6	US-11-097-143-24915 Sequence 24915, A
7	843	13.6	1048	5	US-10-619-992-11 Sequence 11, Appl1
8	611	9.8	522	4	US-10-104-047-3665 Sequence 3665, Ap
9	611	9.8	522	6	US-11-072-512-3665 Sequence 3665, Ap
10	490	7.9	95	3	US-09-867-550-1346 Sequence 1346, Ap
11	311	5.0	67	3	US-09-864-761-48290 Sequence 48290, A
12	267	4.3	276	5	US-10-450-763-41493 Sequence 41493, A
13	208	3.3	1552	5	US-10-330-773-941 Sequence 941, App
14	207	3.3	2377	5	US-10-840-512-196 Sequence 196, App
15	203	3.3	674	6	US-11-096-568A-27755 Sequence 27755, A
16	203	3.3	786	6	US-11-096-568A-27755 Sequence 27755, A
17	203	3.3	1267	4	US-10-092-900A-128 Sequence 6679, Ap
18	200.5	3.2	728	5	US-10-732-923-6679 Sequence 6679, Ap
19	199.5	3.2	639	6	US-11-096-568A-27757 Sequence 27757, A
20	198.5	3.2	3586	4	US-10-334-143-77 Sequence 77, Appl
21	196.5	3.2	1248	4	US-10-437-963-126940 Sequence 126940, A
22	195.5	3.1	123	3	US-09-864-761-42017 Sequence 42017, A
23	195	3.1	2135	4	US-10-288-798-9 Sequence 9, Appl1
24	195	3.1	2135	4	US-10-362-892-9 Sequence 9, Appl1
25	195	3.1	2382	4	US-10-196-935A-2 Sequence 2, Appl1
26	195	3.1	2382	4	US-10-052-648A-40 Sequence 40, Appl
27	195	3.1	2382	4	US-10-336-472-230 Sequence 230, App

28	195	3.1	2382	4	US-10-408-765A-1404 Sequence 1404, Ap
29	195	3.1	2282	6	US-11-009-554-8 Sequence 8, Appl1
30	194.5	3.1	1579	5	US-10-330-773-939 Sequence 939, App
31	193	3.1	2108	5	US-10-491-467-2 Sequence 2, Appl1
32	192.5	3.1	1390	4	US-10-092-900A-224 Sequence 224, App
33	192.5	3.1	1756	5	US-10-450-763-50799 Sequence 50799, A
34	191.5	3.1	2816	4	US-10-240-145-145 Sequence 145, App
35	191.5	3.1	2816	5	US-10-291-128-145 Sequence 145, App
36	191	3.1	1129	5	US-10-840-512-119 Sequence 119, App
37	191	3.1	4462	5	US-10-704-781-3 Sequence 3, Appl1
38	191	3.1	4493	5	US-10-704-781-3 Sequence 3, Appl1
39	190.5	3.1	842	4	US-10-369-493-1940 Sequence 1940, Ap
40	190	3.1	922	4	US-10-437-963-125036 Sequence 125036, A
41	190	3.1	1247	4	US-10-128-714-3473 Sequence 3473, Ap
42	189.5	3.0	2759	5	US-10-450-763-47507 Sequence 47507, A
43	185.5	3.0	1343	4	US-10-408-765A-1085 Sequence 1085, Ap
44	185.5	3.0	2325	4	US-10-663-433-2 Sequence 2, Appl1
45	185	3.0	1340	6	US-11-098-686-11135 Sequence 11135, A

ALIGNMENTS

RESULT 1									
US-09-921-099-2									
Sequence 2, Application US/09921099									
Patent No. US20020107372A1									
GENERAL INFORMATION:									
APPLICANT: Hefeneider, Steven									
APPLICANT: Merkins, Louie									
APPLICANT: Bennett, Robert									
APPLICANT: Seis, Donald									
TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene at									
FILE REFERENCE: 00-617-A									
CURRENT APPLICATION NUMBER: US/09/921, 099									
CURRENT FILING DATE: 2001-08-01									
NUMBER OF SEQ ID NOS: 6									
SOFTWARE: Patent version 3.0									
SEQ ID NO 2									
LENGTH: 1191									
TYPE: PR									
ORGANISM: Homo sapiens									
US-09-921-099-2									
Query Match									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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QY	61	IDVLVFNFFALLDVGAGVDPDHSIKLSNLDENKHYEVAKKCYEDLALYLKPSGKGVAS	120						
DB	61	IDVLVFNFFALLDVGAGVDPDHSIKLSNLDENKHYEVAKKCYEDLALYLKPSGKGVAS	120						
QY	121	INQSAISRPMQKLVTLVNCQVVEEGRVRAAPARSLGERTVTEIILHONPOQISANL	180						
DB	121	INQSAISRPMQKLVTLVNCQVVEEGRVRAAPARSLGERTVTEIILHONPOQISANL	180						
QY	181	MAAVARAGCGFPGPMOEFALKLVLLAEFGSALSKVLFVVOGLERFPQASTSIG	240						
DB	181	MAAVARAGCGFPGPMOEFALKLVLLAEFGSALSKVLFVVOGLERFPQASTSIG	240						
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DB	241	HVVQLLYRASCFKVTTRDESSIMQIKERFSYEALRREHDAQIVHIAEAGLRISPEQW	300						
QY	301	SGLLYGLLAHKHMOIIDKLOSPSPFASVDELITVLOTGDPANLRLPHLELANI	360						
DB	301	SGLLYGLLAHKHMOIIDKLOSPSPFASVDELITVLOTGDPANLRLPHLELANI	360						
QY	361	DNPDAVSPFTWQLENAWAVKTVVHGLVDPIQNSRKCHETPQDPQNSKYTSMCRDRL	420						
DB	361	DNPDAVSPFTWQLENAWAVKTVVHGLVDPIQNSRKCHETPQDPQNSKYTSMCRDRL	420						

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361  DPNPAVSTWQLNANAWAVKTVVHGLVDFIQNSRKHEHPQOPNSKYTSMCRDLR 420
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421  OQGGCPRGNTCTFAISOELEKRYLRNKKINATVTFPLNKVGVNNTTTTAAGVISVI 480
Db      |||
421  OQGGCPRGNTCTFAISOELEKRYLRNKKINATVTFPLNKVGVNNTTTTAAGVISVI 480
Qy      |||
481  GSTETTGKIVPSTNGISNAENSVSOLISRSTSTLRALFTVKVGVGVANGONGAAGPSAD 540
Db      |||
481  GSTETTGKIVPSTNGISNAENSVSOLISRSTSTLRALFTVKVGVGVANGONGAAGPSAD 540
Qy      |||
541  SVTENKIGSPKTPVSNVAATSAAGSNVGTELSVPQKSPFLTRPVYPHSENIQYFQ 600
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541  SVTENKIGSPKTPVSNVAATSAAGSNVGTELSVPQKSPFLTRPVYPHSENIQYFQ 600
Qy      |||
601  DPTQIPFEVPOYPOTGYPPPTVPAGVAPCVPRFVRNNVPESLPASMPYADHYST 660
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601  DPTQIPFEVPOYPOTGYPPPTVPAGVAPCVPRFVRNNVPESLPASMPYADHYST 660
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661  FSPDRMNSPYQPPPOYPGVPPVPSGMVAPVYDSRRIWRPMYQORDIIRSNSLPDM 720
Db      |||
661  FSPDRMNSPYQPPPOYPGVPPVPSGMVAPVYDSRRIWRPMYQORDIIRSNSLPDM 720
Qy      |||
721  DVHSSVYQTSLRERNSLDGYYSVACQPPSEPRITVPLPREPCGHLKTSCEQIRKPD 780
Db      |||
721  DVHSSVYQTSLRERNSLDGYYSVACQPPSEPRITVPLPREPCGHLKTSCEQIRKPD 780
Qy      |||
781  QMAQYHTQAPLVSSITLPVATOSPPTPSPLFVDFPADSESVSCTKFEEDHLSHSPMS 840
Db      |||
781  QMAQYHTQAPLVSSITLPVATOSPPTPSPLFVDFPADSESVSCTKFEEDHLSHSPMS 840
Qy      |||
841  CGTIGSCINAIIDSEPKDVIANNAVLMDISGDVKKRVHLPETORTKEEDPIIPSDGP 900
Db      |||
841  CGTIGSCINAIIDSEPKDVIANNAVLMDISGDVKKRVHLPETORTKEEDPIIPSDGP 900
Qy      |||
901  IISKGAISRSSRTGYHTTDPVQATASQGSATKPIISVSDYVPVNAVDSRMSSYGNATS 960
Db      |||
901  IISKGAISRSSRTGYHTTDPVQATASQGSATKPIISVSDYVPVNAVDSRMSSYGNATS 960
Qy      |||
961  SAHYVERDFITVDSLGHKHSSTGDLLELOQAASNSLLQREANALAMQKNMSLDE 1020
Db      |||
961  SAHYVERDFITVDSLGHKHSSTGDLLELOQAASNSLLQREANALAMQKNMSLDE 1020
Qy      |||
1021  GHMLTLNLKSKELELNGELQSDYTEDATDKPRDIELELSALDDEPQSEPIEILL 1080
Db      |||
1021  GHMLTLNLKSKELELNGELQSDYTEDATDKPRDIELELSALDDEPQSEPIEILL 1080
Qy      |||
1081  DIQGISQNDOLLNGMAVENGHVPVQHQKEPPKQKQSLGEDHVLLEBQKTLIPVTSQF 1140
Db      |||
1081  DIQGISQNDOLLNGMAVENGHVPVQHQKEPPKQKQSLGEDHVLLEBQKTLIPVTSQF 1140
Qy      |||
1141  SQPLPVISINACLPITTSVSAGNLLKTHVMSKNDPLKPVANKMNS 1191
Db      |||
1141  SQPLPVISINACLPITTSVSAGNLLKTHVMSKNDPLKPVANKMNS 1191

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RESULT 2
US-10-619-992-2

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; Sequence 2, Application US/10619992
; Publication No. US20050239163A1
; GENERAL INFORMATION:
; APPLICANT: Hefeneider, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seis, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/10/619,992
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/921,099
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 2
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-619-992-2
Query Match      100.0%; Score 6215; DB 5; length 1191;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1  MEVQAQWTEFLSCIPICINEPDENNHNPISLGCSTHYCTCLNKLHRAKCPFDQAIINTD 60
Db      1  MEVQAQWTEFLSCIPICINEPDENNHNPISLGCSTHYCTCLNKLHRAKCPFDQAIINTD 60
Qy      61  IDVLPVNFALQVQAYPDHOSIKLSNGENKHYEVAKKCYEDALYLKPSGGKVAS 120
Db      61  IDVLPVNFALQVQAYPDHOSIKLSNGENKHYEVAKKCYEDALYLKPSGGKVAS 120
Qy      121  LMQSALSRMQRKLVTLVNCQVVEEGRVAMRAARSIGERTVTBLIQHONPOOLSANTL 180
Db      121  LMQSALSRMQRKLVTLVNCQVVEEGRVAMRAARSIGERTVTBLIQHONPOOLSANTL 180
Qy      181  WAAVBARCGQFLGPMQEBALKVLVLALEDGALSRRKVLVLFVQORLEFRFQASTSIG 240
Db      181  WAAVBARCGQFLGPMQEBALKVLVLALEDGALSRRKVLVLFVQORLEFRFQASTSIG 240
Qy      241  HVVOLLVYRACPKTKRDEDSLSMQLKEEFREYELARRHDAQIVHIAEAGLRISPEQM 300
Db      241  HVVOLLVYRACPKTKRDEDSLSMQLKEEFREYELARRHDAQIVHIAEAGLRISPEQM 300
Qy      301  SSLVYGLDAHKSHMOSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNLRLPHLELANI 360
Db      301  SSLVYGLDAHKSHMOSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNLRLPHLELANI 360
Qy      361  DPNPAVSTWQLNANAWAVKTVVHGLVDFIQNSRKHEHPQOPNSKYTSMCRDLR 420
Db      361  DPNPAVSTWQLNANAWAVKTVVHGLVDFIQNSRKHEHPQOPNSKYTSMCRDLR 420
Qy      421  OQGGCPRGNTCTFAISOELEKRYLRNKKINATVTFPLNKVGVNNTTTTAAGVISVI 480
Db      421  OQGGCPRGNTCTFAISOELEKRYLRNKKINATVTFPLNKVGVNNTTTTAAGVISVI 480
Qy      481  GSTETTGKIVPSTNGISNAENSVSOLISRSTSTLRALFTVKVGVGVANGONGAAGPSAD 540
Db      481  GSTETTGKIVPSTNGISNAENSVSOLISRSTSTLRALFTVKVGVGVANGONGAAGPSAD 540
Qy      541  SVTENKIGSPKTPVSNVAATSAAGSNVGTELSVPQKSPFLTRPVYPHSENIQYFQ 600
Db      541  SVTENKIGSPKTPVSNVAATSAAGSNVGTELSVPQKSPFLTRPVYPHSENIQYFQ 600
Qy      601  DPTQIPFEVPOYPOTGYPPPTVPAGVAPCVPRFVRNNVPESLPASMPYADHYST 660
Db      601  DPTQIPFEVPOYPOTGYPPPTVPAGVAPCVPRFVRNNVPESLPASMPYADHYST 660
Qy      661  FSPDRMNSPYQPPPOYPGVPPVPSGMVAPVYDSRRIWRPMYQORDIIRSNSLPDM 720
Db      661  FSPDRMNSPYQPPPOYPGVPPVPSGMVAPVYDSRRIWRPMYQORDIIRSNSLPDM 720
Qy      721  DVHSSVYQTSLRERNSLDGYYSVACQPPSEPRITVPLPREPCGHLKTSCEQIRKPD 780
Db      721  DVHSSVYQTSLRERNSLDGYYSVACQPPSEPRITVPLPREPCGHLKTSCEQIRKPD 780
Qy      781  QMAQYHTQAPLVSSITLPVATOSPPTPSPLFVDFPADSESVSCTKFEEDHLSHSPMS 840
Db      781  QMAQYHTQAPLVSSITLPVATOSPPTPSPLFVDFPADSESVSCTKFEEDHLSHSPMS 840
Qy      841  CGTIGSCINAIIDSEPKDVIANNAVLMDISGDVKKRVHLPETORTKEEDPIIPSDGP 900
Db      841  CGTIGSCINAIIDSEPKDVIANNAVLMDISGDVKKRVHLPETORTKEEDPIIPSDGP 900
Qy      901  IISKGAISRSSRTGYHTTDPVQATASQGSATKPIISVSDYVPVNAVDSRMSSYGNATS 960
Db      901  IISKGAISRSSRTGYHTTDPVQATASQGSATKPIISVSDYVPVNAVDSRMSSYGNATS 960

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QY 961 SAHYERDRFIYTDLSGHRKHSSTGDLISLEIQAKNSLLIQREANALAMQOKNSLDE 1020
DB 961 SAHYERDRFIYTDLSGHRKHSSTGDLISLEIQAKNSLLIQREANALAMQOKNSLDE 1020
QY 1021 GHLLTLNLISKEIELRNGELSDYTEDADTDPDRDIELELSALDDEPDGSEPIEEL 1080
DB 1021 GHLLTLNLISKEIELRNGELSDYTEDADTDPDRDIELELSALDDEPDGSEPIEEL 1080
QY 1081 DIQLGISQNDQLNGMAVENGHVPVOHQKEPPKOKKSLGSDHVLLEBOKTILPVTSCF 1140
DB 1081 DIQLGISQNDQLNGMAVENGHVPVOHQKEPPKOKKSLGSDHVLLEBOKTILPVTSCF 1140
QY 1141 SQPLPVSISNASCLPITTSVSAGNLLKTHVMSDKNDLKEVANGKMYNS 1191
DB 1141 SQPLPVSISNASCLPITTSVSAGNLLKTHVMSDKNDLKEVANGKMYNS 1191

RESULT 3
US-09-921-099-4
; Sequence 4, Application US/09921099
; Patent No. US20020107372A1
; GENERAL INFORMATION:
; APPLICANT: Hefeneider, Steven
; APPLICANT: Merkinet, Steven
; APPLICANT: Bennett, Robert
; APPLICANT: Seiss, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/09/921, 099
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 1191
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-921-099-4

Query Match 99.9%; Score 6207; DB 3; Length 1191;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEVQAQWTEPLSCPICTNEPDBNHKPIISLGSHTVCTCLNKLHKKACPFDDQAIIND 60
DB 1 MEVQAQWTEPLSCPICTNEPDBNHKPIISLGSHTVCTCLNKLHKKACPFDDQAIIND 60
QY 61 IDVLVFNFLGLVGAQVVDHOSIKLSNKGKHYEVAKKCVEDLALYLKPLSGGKGVAS 120
DB 61 IDVLVFNFLGLVGAQVVDHOSIKLSNKGKHYEVAKKCVEDLALYLKPLSGGKGVAS 120
QY 121 LNSALSRPMQRKLVTLVNCQVEEGRVRAARASLGERVTTELILQHONPOQLSANTL 180
DB 121 LNSALSRPMQRKLVTLVNCQVEEGRVRAARASLGERVTTELILQHONPOQLSANTL 180
QY 181 WAAVBARCGOIFGPAMQEBALKVLIALFDGSLSKVLVLFVQVLEPRFPQASTKTSIG 240
DB 181 WAAVBARCGOIFGPAMQEBALKVLIALFDGSLSKVLVLFVQVLEPRFPQASTKTSIG 240
QY 241 HVOVLVLRASCFKMTKRDSDSSIMOLKEPRFSEALARRHDDQIVHIAEAGRISPEQM 300
DB 241 HVOVLVLRASCFKMTKRDSDSSIMOLKEPRFSEALARRHDDQIVHIAEAGRISPEQM 300
QY 301 SSLLVGLDLAKHSMOSIIDKLOS PESFAKVOELTIVLQRTGDPANLRLRPHLELLANI 360
DB 301 SSLLVGLDLAKHSMOSIIDKLOS PESFAKVOELTIVLQRTGDPANLRLRPHLELLANI 360
QY 361 DNPDPVASTTWQOLENAMAAYKTIVHGLVDFTONYSRKHGHPQOPPNKTKTSMCRDLR 420
DB 361 DNPDPVASTTWQOLENAMAAYKTIVHGLVDFTONYSRKHGHPQOPPNKTKTSMCRDLR 420
QY 421 OQGGCPRGNTCTFAHSQELKRYLRNKKINATVTFPPLINKGVNNTVTTAGNVISYI 480
DB 421 OQGGCPRGNTCTFAHSQELKRYLRNKKINATVTFPPLINKGVNNTVTTAGNVISYI 480

DB 421 OQGGCPRGNTCTFAHSQELKRYLRNKKINATVTFPPLINKGVNNTVTTAGNVISYI 480
QY 481 GSTETTGKIVPSTNGISNAENSVSOLISRSIDSTLPALETYKVKGVANGVANGQNAAGPSAD 540
DB 481 GSTETTGKIVPSTNGISNAENSVSOLISRSIDSTLPALETYKVKGVANGVANGQNAAGPSAD 540
QY 541 SVTENKIGSPKTPVSNVAATSAGPSNVTGLNSVPKOSPFILTRVPVYPHSENIQYQO 600
DB 541 SVTENKIGSPKTPVSNVAATSAGPSNVTGLNSVPKOSPFILTRVPVYPHSENIQYQO 600
QY 601 DPTQIPEFVPOYPQYGVPPPTVPAGVAPCVPRFVRNNPPESSLPASMPYADHYST 660
DB 601 DPTQIPEFVPOYPQYGVPPPTVPAGVAPCVPRFVRNNPPESSLPASMPYADHYST 660
QY 661 FSPDRMNSPYQPPPOPGYGVPPVPSGMVAPVYDSRIIMPPMYQORDIIRSNLPPM 720
DB 661 FSPDRMNSPYQPPPOPGYGVPPVPSGMVAPVYDSRIIMPPMYQORDIIRSNLPPM 720
QY 721 DVMHSSVYQTSIREYNSLDGYVSAACOPSPSPRTTVPLEPRPCGHLKTSCEBQIRKRP 780
DB 721 DVMHSSVYQTSIREYNSLDGYVSAACOPSPSPRTTVPLEPRPCGHLKTSCEBQIRKRP 780
QY 781 QMAQYHTOKAPVSSSTLPVATOSPPTPSPPLFSDVFRADFSSESVSCTKFEEDHLSHYSPMS 840
DB 781 QMAQYHTOKAPVSSSTLPVATOSPPTPSPPLFSDVFRADFSSESVSCTKFEEDHLSHYSPMS 840
QY 841 CGTIGSCINADISEPKDVIANNAVIMDIDSGDVKRVHLEFTRTKEDPPIIPSDGP 900
DB 841 CGTIGSCINADISEPKDVIANNAVIMDIDSGDVKRVHLEFTRTKEDPPIIPSDGP 900
QY 901 IISKMGATSRSSRTGYHTTDPVOATASOGSARKPISVSYPVYVYVAVDVRMSYNGEATS 960
DB 901 IISKMGATSRSSRTGYHTTDPVOATASOGSARKPISVSYPVYVYVAVDVRMSYNGEATS 960
QY 961 SAHYERDRFIYTDLSGHRKHSSTGDLISLEIQAKNSLLIQREANALAMQOKNSLDE 1020
DB 961 SAHYERDRFIYTDLSGHRKHSSTGDLISLEIQAKNSLLIQREANALAMQOKNSLDE 1020
QY 1021 GHLLTLNLISKEIELRNGELSDYTEDADTDPDRDIELELSALDDEPDGSEPIEEL 1080
DB 1021 GHLLTLNLISKEIELRNGELSDYTEDADTDPDRDIELELSALDDEPDGSEPIEEL 1080
QY 1081 DIQLGISQNDQLNGMAVENGHVPVOHQKEPPKOKKSLGSDHVLLEBOKTILPVTSCF 1140
DB 1081 DIQLGISQNDQLNGMAVENGHVPVOHQKEPPKOKKSLGSDHVLLEBOKTILPVTSCF 1140
QY 1141 SQPLPVSISNASCLPITTSVSAGNLLKTHVMSDKNDLKEVANGKMYNS 1191
DB 1141 SQPLPVSISNASCLPITTSVSAGNLLKTHVMSDKNDLKEVANGKMYNS 1191

RESULT 4
US-10-619-992-4
; Sequence 4, Application US/10619992
; Publication No. US20050239163A1
; GENERAL INFORMATION:
; APPLICANT: Hefeneider, Steven
; APPLICANT: Merkinet, Steven
; APPLICANT: Bennett, Robert
; APPLICANT: Seiss, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/10/619, 992
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/921, 099
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 1191
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-619-992-4

Query Match 99.9%; Score 6207; DB 5; Length 1191;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MPVQAQWTEFLSCPICYNEFDENVAKPISLGCSTHVCCTCLNKLHRAKCPFDQTAINTD 60
DB 1 MAVQAQWTEFLSCPICYNEFDENVAKPISLGCSTHVCCTCLNKLHRAKCPFDQTAINTD 60
OY 61 IDVLVFNFALLQVGAQVDPDHOSIKLSNKGKHYEVAKKCVEDLALYIKPLSGKGAVAS 120
DB 61 IDVLVFNFALLQVGAQVDPDHOSIKLSNKGKHYEVAKKCVEDLALYIKPLSGKGAVAS 120
OY 121 LNSQALSRPMOKRLVTLVNCQVVEEGRVRAARAASLGERVTYTELILQHNPOOLSANTL 180
DB 121 LNSQALSRPMOKRLVTLVNCQVVEEGRVRAARAASLGERVTYTELILQHNPOOLSANTL 180
OY 181 MAABARCGOFLGPMQOEALKVLVLLALEDGSLSRKVLVLFVQRLERFPQASKTSG 240
DB 181 MAABARCGOFLGPMQOEALKVLVLLALEDGSLSRKVLVLFVQRLERFPQASKTSG 240
OY 241 HVOVLLYRASCFKVTYKRDSSIMQKEFRSYEARREHDAQIVHIAEAGLRISPEQW 300
DB 241 HVOVLLYRASCFKVTYKRDSSIMQKEFRSYEARREHDAQIVHIAEAGLRISPEQW 300
OY 301 SSLVYGDIAHKSHMOSIIDKLOSPEFASVOELTIVLQRTGDPANLNLRLPHELLANI 360
DB 301 SSLVYGDIAHKSHMOSIIDKLOSPEFASVOELTIVLQRTGDPANLNLRLPHELLANI 360
OY 361 DENPDVSPTEWOLENAMVAVKTVVHGLVDFIQNSRKCHETPOPOPNSKYKTSWCRDLR 420
DB 361 DENPDVSPTEWOLENAMVAVKTVVHGLVDFIQNSRKCHETPOPOPNSKYKTSWCRDLR 420
OY 421 OQGGCGRGNTCTPFAHQEELKYLRLNKKINATVTRFPLNKVGVNNTVTTAGNIVSYI 480
DB 421 OQGGCGRGNTCTPFAHQEELKYLRLNKKINATVTRFPLNKVGVNNTVTTAGNIVSYI 480
OY 481 GSTETTGKIVPSTNGISNAENSVSQILSRSTDTLALSTVKKVGKANGONGAAPSAD 540
DB 481 GSTETTGKIVPSTNGISNAENSVSQILSRSTDTLALSTVKKVGKANGONGAAPSAD 540
OY 541 SVTENKISGPKTPVSNVAATSAGPSNVGTSLNSVQKSPFLTRVPVYPHSENIQYRQ 600
DB 541 SVTENKISGPKTPVSNVAATSAGPSNVGTSLNSVQKSPFLTRVPVYPHSENIQYRQ 600
OY 601 DRTQIPFEVPOYPOTGYRPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST 660
DB 601 DRTQIPFEVPOYPOTGYRPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST 660
OY 661 FSPRDMNSSPYQPPPOPYGVPVPVPSGMVYAPVYDSRRIWPPMYQORDIIRSNGLPPM 720
DB 661 FSPRDMNSSPYQPPPOPYGVPVPVPSGMVYAPVYDSRRIWPPMYQORDIIRSNGLPPM 720
OY 721 DVWHSVYQTSLRERYSNLDGYYSVACQPPSEBRTTVPLPREBCGLKTSCEBQIRKPD 780
DB 721 DVWHSVYQTSLRERYSNLDGYYSVACQPPSEBRTTVPLPREBCGLKTSCEBQIRKPD 780
OY 781 QMAQYHTQAPLVSSTLPAVATOSPTPSPSLFSYDFADPSESYSYGKFEEDHLSHSPMS 840
DB 781 QMAQYHTQAPLVSSTLPAVATOSPTPSPSLFSYDFADPSESYSYGKFEEDHLSHSPMS 840
OY 841 CGTIGSCINAIIDBRPDVIANSNVAMLDSDGPKSRVHLFETQRTKEDPIIPPSDGP 900
DB 841 CGTIGSCINAIIDBRPDVIANSNVAMLDSDGPKSRVHLFETQRTKEDPIIPPSDGP 900
OY 901 IISKWCAISRSRTGYHTTDPVQATASQGSATKPIISVDYVPVYNAVADRSWSSYGNEATS 960
DB 901 IISKWCAISRSRTGYHTTDPVQATASQGSATKPIISVDYVPVYNAVADRSWSSYGNEATS 960
OY 961 SAHYVERDRFIVTDLSGHRKHSSTGDLLELOAKSNSTLLQREANALAMQKMSLDB 1020
DB 961 SAHYVERDRFIVTDLSGHRKHSSTGDLLELOAKSNSTLLQREANALAMQKMSLDB 1020

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OY 1021 GRHLTLNLISKEIEIRNGELQSDYTEADTDYKPRDIDIELLSALDTDEPDGQSEPIEIL 1080
DB 1021 GRHLTLNLISKEIEIRNGELQSDYTEADTDYKPRDIDIELLSALDTDEPDGQSEPIEIL 1080
OY 1081 DIQIGISSONQDOLNGMAVENGHPIVQOHQKEPPKXKQSGSDHYTLEEQKTLIPPTSCE 1140
DB 1081 DIQIGISSONQDOLNGMAVENGHPIVQOHQKEPPKXKQSGSDHYTLEEQKTLIPPTSCE 1140
OY 1141 SOPLPVSIISNASCPLPITTSVSAGNLIILKTHVMSDEKNDPLKRVANGKWNVS 1191
DB 1141 SOPLPVSIISNASCPLPITTSVSAGNLIILKTHVMSDEKNDPLKRVANGKWNVS 1191

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RESULT 5

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US-10-485-225-8
; Sequence 8, Application US/10485225
; Publication No. US20050181355A1
; GENERAL INFORMATION:
; APPLICANT: Greener, Tavika
; APPLICANT: Moskowitz, Haim
; APPLICANT: Reiss, Yuval
; APPLICANT: Alroy, Iris
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE OF INVENTION: MODULATION OF VIRAL MATURATION
; FILE REFERENCE: PROL-P02-001
; CURRENT APPLICATION NUMBER: US/10/485,225
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/308,958
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/345,846
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1048
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-225-8

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Query Match 88.2%; Score 5483; DB 5; Length 1048;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MPVQAQWTEFLSCPICYNEFDENVAKPISLGCSTHVCCTCLNKLHRAKCPFDQTAINTD 60
DB 1 MPVQAQWTEFLSCPICYNEFDENVAKPISLGCSTHVCCTCLNKLHRAKCPFDQTAINTD 60
OY 61 IDVLVFNFALLQVGAQVDPDHOSIKLSNKGKHYEVAKKCVEDLALYIKPLSGKGAVAS 120
DB 61 IDVLVFNFALLQVGAQVDPDHOSIKLSNKGKHYEVAKKCVEDLALYIKPLSGKGAVAS 120
OY 121 LNSQALSRPMOKRLVTLVNCQVVEEGRVRAARAASLGERVTYTELILQHNPOOLSANTL 180
DB 121 LNSQALSRPMOKRLVTLVNCQVVEEGRVRAARAASLGERVTYTELILQHNPOOLSANTL 180
OY 181 MAABARCGOFLGPMQOEALKVLVLLALEDGSLSRKVLVLFVQRLERFPQASKTSG 240
DB 181 MAABARCGOFLGPMQOEALKVLVLLALEDGSLSRKVLVLFVQRLERFPQASKTSG 240
OY 241 HVOVLLYRASCFKVTYKRDSSIMQKEFRSYEARREHDAQIVHIAEAGLRISPEQW 300
DB 241 HVOVLLYRASCFKVTYKRDSSIMQKEFRSYEARREHDAQIVHIAEAGLRISPEQW 300
OY 301 SSLVYGDIAHKSHMOSIIDKLOSPEFASVOELTIVLQRTGDPANLNLRLPHELLANI 360
DB 301 SSLVYGDIAHKSHMOSIIDKLOSPEFASVOELTIVLQRTGDPANLNLRLPHELLANI 360
OY 361 DENPDVSPTEWOLENAMVAVKTVVHGLVDFIQNSRKCHETPOPOPNSKYKTSWCRDLR 420
DB 361 DENPDVSPTEWOLENAMVAVKTVVHGLVDFIQNSRKCHETPOPOPNSKYKTSWCRDLR 420
OY 421 OQGGCGRGNTCTPFAHQEELKYLRLNKKINATVTRFPLNKVGVNNTVTTAGNIVSYI 480
DB 421 OQGGCGRGNTCTPFAHQEELKYLRLNKKINATVTRFPLNKVGVNNTVTTAGNIVSYI 480

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Db 421 OGGCGRCNCTFAHSGELEKRYLRKKNKINATVTFPLINKGVNNTVTTAGNIVSI 480
Qy 481 GSTETTGKIVPSTNGISNAENSVSOLISRSTDSLRALETVKVKGVGANGONAGPSAD 540
Db 481 GSTETTGKIVPSTNGISNAENSVSOLISRSTDSLRALETVKVKGVGANGONAGPSAD 540
Qy 541 STENKISGPPKTPVSNVAATISAGPSNVGTELSNSVQKSSPLTRPVYPRHSENIQYRQ 600
Db 541 STENKISGPPKTPVSNVAATISAGPSNVGTELSNSVQKSSPLTRPVYPRHSENIQYRQ 600
Qy 601 DRTQIPFEPVPOYPOTGYPPPPPTPAGVAPCVPRVFRNNVPBESSLPASHPYADHYST 660
Db 601 DRTQIPFEPVPOYPOTGYPPPPPTPAGVAPCVPRVFRNNVPBESSLPASHPYADHYST 660
Qy 661 FSPRDRMNSSPYQPPPPQYGPVPVPSGMVAPVYDSRRIWRPMPYQORDIIRSNSLPMP 720
Db 661 FSPRDRMNSSPYQPPPPQYGPVPVPSGMVAPVYDSRRIWRPMPYQORDIIRSNSLPMP 720
Qy 721 DVHSSVYQTSLRERYNSLDGYVVAOCOPSPSPRTVPLPREPCGHLTKTSCBQIRKPD 780
Db 721 DVHSSVYQTSLRERYNSLDGYVVAOCOPSPSPRTVPLPREPCGHLTKTSCBQIRKPD 780
Qy 781 QMAQHTOKAPVSSITLPATOSPFPSPPLFSVDPRADSESYSCTKFEEDHLSHSPMS 840
Db 781 QMAQHTOKAPVSSITLPATOSPFPSPPLFSVDPRADSESYSCTKFEEDHLSHSPMS 840
Qy 841 CGTIGSCINAIIDSEPKDVIANSNAVLMDLSDGVKRRVHLEFQRTKEDPIIPSDGP 900
Db 841 CGTIGSCINAIIDSEPKDVIANSNAVLMDLSDGVKRRVHLEFQRTKEDPIIPSDGP 900
Qy 901 IISKGAISRSSRTGHTTDPVQATASQGSATKPIVSIVPVYVAVNADSRMSYGNARS 960
Db 901 IISKGAISRSSRTGHTTDPVQATASQGSATKPIVSIVPVYVAVNADSRMSYGNARS 960
Qy 961 SAHYERDRFITDLSGHRKHSSTGDLSTELQAKNSLLOREANALAMOOKNSLDE 1020
Db 961 SAHYERDRFITDLSGHRKHSSTGDLSTELQAKNSLLOREANALAMOOKNSLDE 1020
Qy 1021 GRHLTLNLKSKEIELANGELQSDYTEDA 1048
Db 1021 GRHLTLNLKSKEIELANGELQSDYTEDA 1048

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; SOFTWARE: FastSBO for Windows version 4.0
; SEQ ID NO 24915
; LENGTH: 819
; TYPE: PRT
; ORGANISM: DROSOPHILA
; US-11-097-143-24915

Query Match      24.7%; Score 1338; DB 6; Length 819;
Best Local Similarity 40.5%; Pred. No. 2.1e-97;
Matches 386; Conservative 98; Mismatches 226; Indels 242; Gaps 29;

1 1MPVOAOWTEFAPICVYEPDENVHKPISLCSHPTVCCTCNLKRKACPQDQAIINTD 60
Db 1 1MPVOAOWTEFAPICVYEPDENVHKPISLCSHPTVCCTCNLKRKACPQDQAIINTD 60
Qy 61 IDVLVFNFALLQV-----GAQVPHQSIKLSNIGENKHYEAKKCVEDALATLKEP 112
Db 61 IDVLVFNFALLQV-----GAQVPHQSIKLSNIGENKHYEAKKCVEDALATLKEP 112
Qy 113 SGKGVALNSGALSRLPMQRLVTLVNCQVVEBGRVARMARASIGERTYTELIIQHON 172
Db 113 INLNG-----NGMLTRPMLRKLVTLVNCOIMEBGRVRLRARASIGERTYTELIIQHON 173
Qy 173 POOLSANLMAAARVARGCOPIAGPAMOEALKVLIALLEDGSALSRLKVLVFNVQRLPREP 232
Db 174 POOLSANLMAAARVARGCOPIAGPAMOEALKVLIALLEDGSALSRLKVLVFNVQRLPREP 233
Qy 233 QASKTSIGHVQVLLVYRASCFCYTKDEDSJLMQLEEFPSYEALRREHDAQIVHAMEAG 292
Db 234 QASKTSIGHVQVLLVYRASCFCYTKDEDSJLMQLEEFRTYDALRREHDAQIVHATEAG 293
Qy 293 LRISEPOWSSLLYGDLAHSHMOIITDKLQSPESPAKSYQELTIVLQRTGDPANLRLRP 352
Db 294 LRIAPBOWSSLLYGVVHSHMOIITDKLQTPSSFAQSVQELVIALQRTSDPAKSSLHH 353
Qy 353 HLELLANIDPNDAVSPTWEOLENMAVAVTVHGLVDTIONYS-RK-----GHETPQ 404
Db 354 HUKYLANIDPCAE-VAP-MSVLAEDADVAHSHVGLVNLQHHGVKADGISGCGSSGCT 411
Qy 405 POPNSKYKTSMCRDLRQGGCPCRTNCTPFAHSGELEKRYLRKKNKINATVTFPLINKVG 464
Db 412 TNSNPKYKISLCRDNLNVRVRCRGSCTFAHSGELEVRYRANR----- 465
Qy 465 VNNVTTTAGNVISVIGSTETTGKIVPSTNGISNAENSVSOLISRSTDSLRALETVKYV 524
Db 466 ----- 455
Qy 525 GRVGANGONAGPSADSVTENKISGPPKTPVSNVAATISAGPSNVGTELSVP--OKSSPP 582
Db 466 -----GKMKTPLA-----LOGPRAVGVGAIKKPPLGEBQGRP 487
Qy 583 LTRVPVYPRHSENIQYFODPRTQIPPEVPOYQOTGYPPPPPTPAGVAPCVPRFVSNNV 642
Db 488 LGNMPMLPMSD-MHYMGSPR-----GYLDP-----SLGLSP-----CGGL 522
Qy 643 PESSLEPPAS---MP---YADHYSTF---SPRDRMNSSPYQPPPPQYGPVPVPSGMVAPV 654
Db 523 PSHHSPIITRLIVPSRYSDFSGFGGCTPR-----IFPREYQANPVAA----- 566
Qy 655 YDSRRIWRPMPYQORDIIRSNLSLPPM---DVHSSVYQTSLRERYNSLDGYVVAOCOPP- 750
Db 567 --TORVANPNSVNSNLHKGYMLPASGVDVHFLA-----NPMQDAYIAQOQHPP 614
Qy 751 -----SEPTVPLPREPCGHLTKTSCBQ-IRKPDQMAQYHTOKAPVLS-STLPATOS 803
Db 615 QHPQOQPPSSKPNPSRPLSILPATADTSFPEKKPPNSVIDLDRVBEVNVADVPLFRSS 674
Qy 804 PTPPSPPLFSVDPRADSESYSCTKFEEDHLSHSPMSCTGSCINAIIDSEPKDVIANSV 863
Db 675 -----NNNNNNNNNSNNNNNNNGSSLSLFVN-NTGKDSANFVNS---DSILDDO 720
Qy 864 AVIAMDLSGDVVRKRVHLEFQRTKEDPIIPSDPIISKGAISRSSRTG 915

```

Db 721 ASTFDPVTGSSMLSIY-----GPICPK-----SETTG 747

RESULT 7
US-10-619-992-11
; Sequence 11, Application US/10619992
; Publication No. US20050239163A1
; GENERAL INFORMATION:
; APPLICANT: Hefeneider, Steven
; APPLICANT: Hefeneider, Steven
; APPLICANT: Bennett, Robert
; APPLICANT: Bennett, Robert
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/10/619, 992
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/921,099
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent version 3.0
; SEQ ID NO 11
; LENGTH: 1048
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-619-992-11

Query Match 13.6%; Score 843; DB 5; Length 1048;
Best Local Similarity 30.6%; Pred. No. 5,4e-49;
Matches 238; Conservative 99; Mismatches 278; Indels 162; Gaps 23;

QY 4 QAAWTEFLSCPICYNEFDENVHKKPISLGSHTVCKTCKLNR--KACPFDTAINTDI 61
DB 6 QGGQHQEVLCSICNRHFNH-TFLPVSILGHVYICKAKKRENOJCKPCPHDMKTTTSP 64
QY 62 DVLPNVFNALLQVGAOVPRHOSIKLSNLSBNKHYEAKKCEDLALYLKPLSGGKVASL 121
DB 65 SEYPPNVALLSVY---FPRKQCTWLSGAVSEAEKRDQSLQ-IAKFFREADSERG-GTV 119
QY 122 NOSALSRPMQRLVTLVNCQLVEBGRVAMRAARSLGERTVTELLIQONPOQLSANIM 181
DB 120 SREISRTLOKRYKALLCYQMRVDRKLTLMKCRGISERWMEIILISIOSNTHVSQIM 179
QY 182 AAVRARGCQFLPAMQGEALKVLTLALBDGALSRLKVLVFNVOQLRPPFQASKTISGH 241
DB 180 SAVRARGCQFLPAMQDDVLRLIMLTLETGECIARKNLVVVQTLASDYPQVSKTCVGH 239
QY 242 VVQLYRACCFKTKRDEDESSLMQLEKFRSYALAREHDAQVHIAAMEAGLISFEQMS 301
DB 240 VVQLYRACCFKTKRDEDESSLMQLEKFRSYALAREHDAQVHIAAMEAGLISFEQMS 299
QY 302 SILYGDLAHSHMQSIIDKLQSPSPAKSVQELTIVLQRTGDPAN-----LNRLRP 352
DB 300 ALLYADQSHRSHMQSIIDKLQSPSPAKSVQELTIVLQRTGDPAN-----LNRLRP 356
QY 353 HUELLANIDPNDAVSPTEQOLENANAVKTVVHGLVDFIQNY---SRKHETPOQPNIS 409
DB 357 CLEFPAIGIEHEDTSMKMGIDALHQLRLK--LHGQDILRKMPKEBGRGVILQAEVPGG 414
QY 410 KYKTSKCRDLRQGGCPRGTNCTFAHSQEBLEKRYLRANKKINATVATFPLNKVGNNTV 469
DB 415 -----MGGGPGGSG-----GAEGRI----- 430
QY 470 TTTAGNVISVISTETTKIIVPSTNGISNAENSVSLISNSTDTSLRALETVKGVKVG 529
DB 431 -----GGHLHPYISOIDETGKISRTNPKDNSHNSPO----- 461
QY 530 NGQNAAGPSADSVTEKTKISPPKTPVSNVAATSGASNVGTETLSVPOKSSPFLTRVPY 589
DB 462 -----TPPKQPRQKRYQMGIPENRMG-----YSDAPFPIPSHQOQ 497
QY 590 PPHSENIOYFQDPRTOIPREVPOYPOTGYPPPPPTVPAGVAPVPPFVSNVNPBESSLP 649
DB 498 PPP-----OFFNS--OHLPRFRGRQRGAPPPPPPP-----MPLIGVD-----MPG 539

QY 650 ASMPYADHYSTFSPDRMNSP-----YQPPQPYGVPVPSGMYAPVDSRRIRWPP 704
DB 540 AFMMQATEVLTL-ADQGMVNGTPQRVIMQSPHLLGGPVMVLPQGMVPPQSMTPVGGP 598
QY 705 MYQRDDIIRSNLSPMDVMHSSV-YQTSIREKYNLSLDGYSV---ACQPSSEPTTV 757
DB 599 M-----GEMGMPVPSIPVQVPEPNTMTATSPGVSITYPAASPPQPPHTI 643

RESULT 8
US-10-104-047-3665
; Sequence 3665, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 3665
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3665

Query Match 9.8%; Score 611; DB 4; Length 522;
Best Local Similarity 34.1%; Pred. No. 2,3e-33;
Matches 187; Conservative 76; Mismatches 187; Indels 98; Gaps 27;

QY 618 YTPPPPTVAGVAPCYPRRVRSNNVPBESSLPASMYADHYSTFSPDRMNSPYPQPP 677
DB 2 YTPPP-----QCVRFRV---PPSAPBPAPYLDHYPPYL-QERVNSQGTQPO 49
QY 678 QYGPAPVPVSGMYAPVYDSRRIMRPMYQDDIIRSNLSPMDVMHSSV---YQTSIRER 735
DB 50 Q-----YPPY-----YPSHYDGRVYPAVSTREIFPESP1-PIETPPAVPSVPSRRR 100
QY 736 YNSLDGYSVACOP-----DS-----EPRTVPLPREBCGLKTSCEQIRKRPQMAQYHT 787
DB 101 YQIESYVYVAHPHQIRPSYLRPEPYSRLPPPPOP-----HSLDELHRRKKEIMAQLEB 156
QY 788 QKAPLVSTLPVATQSPPTPSPPLFSVDFRADSESYSQTKFEEDHLSHSPSCGTIGSC 847
DB 157 RK---VISPPPPA-PSPTLP-PTFHEEFLBEDLKVAG-KYKANDYSQYSPMSCTTIGST 210
QY 848 INAIDSEPDQVANSNAVLMDLSDGVKRRVHLFETQRTKE--EDPIIPFSDGPIISKW 905
DB 211 IGTQAKPKPDVVAAGSVEMMANYSKGM--RDQRLDQRAAETSDDLLPFGDRPTVSRF 268
QY 906 GAISRSRTGYHTTDPVQATASQSGATKPIVSVDYVYVNAVDSRY--SSYG--NEATSS 961
DB 269 GAISRTSKTIYQAGQPMQAPQGAFTKISINISDVSFY--GTHGCGASPYSPHONI 936
QY 962 AHYVERDRITVNDLSHRK--HSTGDLJSLLEQ-----AKSNSLLOR 1004
DB 327 GHFSERERISMSVASHGRPLPSAREQRLLEQLQNLHOISQOTQLRGPAANSNRLVLRQ 386
QY 1005 EANAALMQO-----KNNSLDEGRHLTLNL--LSKEIELRNGELQSDYTEDATDKPD 1054
DB 387 EANTLAGQOPPPPPPKPMGMSQGLDELHQVRELIGKTRRELISM--NQSLSLMK-- 443
QY 1055 RILELESLALDDE--PDQSQSEPIETLIDIQGISQNDQLNGMAVENGHVYQCHQKEP 1112
DB 444 -----SKLNTSKQALENQEPONKV-----PAEDLTLTFSDVPNGSALTQENISL 488
QY 1113 PKQKQSL 1120
DB 489 LSNKTSLSL 496

RESULT 9

US-11-072-512-3665
; Sequence 3665, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARA, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 08435-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3665
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3665

Query Match 9.8%; Score 611; DB 6; Length 522;

Best Local Similarity 34.1%; Pred. No. 2,3e-33;

Matches 187; Conservative 76; Mismatches 187; Indels 98; Gaps 27;

QY 618 YTPPTVPAGVACVPRFVRSNNVPESSLPASMPYADHYSTFSPRDMSSPYQPPPP 677
DB 2 YTPPP-----QCVRFR-----PPSAPPAPPYLDHYPPYL-QERVNNSQYGTQPO 49
QY 678 QPYGVPPVPSGMVAPVYDSRKIMRPMWQDDIIRNSLPRMDVHSSV--YQTSLR 735
DB 50 Q-----YPPI-----YPSHYDGRVYPAPSYTREIFRESPI-PIEIPPAVPSVPSRER 100
QY 726 YNSLDGYSVACQ-----PS-----EPRTVPLPREPCGHLKTSCEQIRKRPDQWQYNT 787
DB 101 YQGISYYPVAHHPQIRBSYRREPPYSKLP PPPQ-----HSLDELHRRKREINAAOLEE 156
QY 788 OKAPLVSTLPVATOSPPTPSPLFVSDFPADSESYSVGTKEFDHLSHYSPWSCGTIGSC 847
DB 157 RK---VISPPPPA-PSPTLP-PTFHEBEFLDEDLKAG-KYGNQDYSQSPSCDTIGSY 210
QY 848 INALISEPVDVANSNAVLMDIDSGDVKKRVHLFETQRTK--EDPIIPESDGPILSK 905
DB 211 IGTKAKKPDVVAAGSVEMNNVESKGM--RDQRLDQRAAFTSDDDLIPFGRPTVSRF 268
QY 906 GAISRSRTGYHTTDPVQATASQGSATKPISVSDVYPYNAVDSRW--SSYG--NEATSS 961
DB 269 GAISTSTKITTYGAGPMQMAPQAGATKSNISDSIPY--GTHGNGASPYPHQNIIBQ 326
QY 962 AHYVERDREITVDLGGHRK--HSTGDLISLEIQ-----AKSNLLIOR 1004
DB 327 GHFSRERISMSBVASHGKPLPSAEREQLRLQLQINHQISOOTQLRGPEAVSNRLVLR 386

QY 1005 EANALAMQ-----KWNLSDEGRHLTANT--LSKEIELNGEIOSDYTEDATDTPKD 1054
DB 387 EANTLAGOSQPPPPPPKPMGMISSQSLBELHQVREIKRKTRELISM--NCCSLDMK-- 443
QY 1055 RDIELELSALDTE--PDGQSEPIEILDIQGLISSQNDQLNGAVENGHPVQHQKEP 1112
DB 444 -----SKLNTSKOAEHQPEPQNV-----PAEDLTLTFSVDPNGSALTQENISL 488
QY 1113 PKQKKQSL 1120
DB 489 LSNKTSSTL 496

RESULT 10

US-09-867-550-1346
; Sequence 1346, Application US/09867550
; Patent No. US2002008206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad.
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US2002008206A1 Polynucleotides from Atherogenic Cells and
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1346
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-1346

Query Match 7.9%; Score 490; DB 3; Length 95;

Best Local Similarity 100.0%; Pred. No. 4.1e-26;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1097 MAVENGHPVQHQKPPPKQKQSLGPDHYILEOKTILPVTSQFSQPLVSNASCPLPI 1156
DB 1 MAVENGHPVQHQKPPPKQKQSLGPDHYILEOKTILPVTSQFSQPLVSNASCPLPI 60
QY 1157 TTSVAGNLLIKTHVMSDDKNDFLKPVANGKXVNS 1191
DB 61 TTSVAGNLLIKTHVMSDDKNDFLKPVANGKXVNS 95

RESULT 11

US-09-864-48290
; Sequence 48290, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04

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1  PRIOR APPLICATION NUMBER: US 60/236,359
2  PRIOR FILING DATE: 2000-09-27
3  PRIOR APPLICATION NUMBER: PCT/US01/00666
4  PRIOR FILING DATE: 2001-01-30
5  PRIOR APPLICATION NUMBER: PCT/US01/00667
6  PRIOR FILING DATE: 2001-01-30
7  PRIOR APPLICATION NUMBER: PCT/US01/00664
8  PRIOR FILING DATE: 2001-01-30
9  PRIOR APPLICATION NUMBER: PCT/US01/00669
10 PRIOR FILING DATE: 2001-01-30
11 PRIOR APPLICATION NUMBER: PCT/US01/00665
12 PRIOR FILING DATE: 2001-01-30
13 PRIOR APPLICATION NUMBER: PCT/US01/00668
14 PRIOR FILING DATE: 2001-01-30
15 PRIOR APPLICATION NUMBER: PCT/US01/00663
16 PRIOR FILING DATE: 2001-01-30
17 PRIOR APPLICATION NUMBER: PCT/US01/00662
18 PRIOR FILING DATE: 2001-01-30
19 PRIOR APPLICATION NUMBER: PCT/US01/00661
20 PRIOR FILING DATE: 2001-01-30
21 PRIOR APPLICATION NUMBER: PCT/US01/00670
22 PRIOR FILING DATE: 2001-01-30
23 PRIOR APPLICATION NUMBER: US 60/234,687
24 PRIOR FILING DATE: 2000-09-21
25 PRIOR APPLICATION NUMBER: US 09/608,408
26 PRIOR FILING DATE: 2000-06-30
27 PRIOR APPLICATION NUMBER: US 09/774,203
28 PRIOR FILING DATE: 2001-01-29
29 NUMBER OF SEQ ID NOS: 49117
30 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
31 SEQ ID NO 48290
32 LENGTH: 67
33 TYPE: PRT
34 ORGANISM: Homo sapiens
35 FEATURE:
36 OTHER INFORMATION: MAP TO AL136170.2
37 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
38 OTHER INFORMATION: SWISSPROT HIT: M091570, EVALU 2.60e+00
39 OTHER INFORMATION: EST_HUMAN HIT: AM962574.1, EVALU 4.00e-32
40 US-09-864-761-48290

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Only Match          5.0%; Score 311; DB 3; Length 67;
Best Local Similarity 89.6%; Pred. No. 6,4e-14;
Matches 60; Conservative 5; Mismatches 2; Indels 0; Gaps 0

OY      254 VTKRDEDSLMLQKEEPRSYEARLRREHDAQIVIMEAGLRISPEQWSSLVGYDLAKHSH 313
          |||
Db      1 VTKDEDSLSMLQKEEPRSYEARLRREHDSQIVIMEAGLRISPEQWSSLVGYDQSHKSH 60

OY      314 MOSIIDK 320
          |||
Db      61 MOSIIDK 67

RESULT 12
US-10-450-763-41493
; Sequence 41493, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 41493

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```

: LENGTH: 276
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (63)..(105)
: OTHER INFORMATION: Ribosomal protein L30e proteins domain identified by eMATRIX,
: OTHER INFORMATION: accession number BL00709B, p-value=5.313e-28, raw score of 21.58
: FEATURE:
: NAME/KEY: DOMAIN
: LOCATION: (171)..(201)
: OTHER INFORMATION: Zinc finger, C3HC4 type (RING finger) domain identified by
: OTHER INFORMATION: Pfam, accession name zf-C3HC4, E-value=0.014, Pfam score of 12.6
US-10-450-763-41#93

```

Query Match	4.3%	Score 267;	DB 5;	Length 276;
Best Local Similarity	59.8%	Pred. No. 6.5e-10;		
Matches 52;	Conservative 9;	Mismatches 10;	Indels 16;	Gaps 2.

QY	8	WTEFLSPICVNEFDENVHKKPISLGSCHTVCCTKLNRKACFPDQTAINTDIDLEPVN	67
		:	
Db	168	WT-----PDETIKRPISLGGCHTVCCKMLNLRKACFPDQTTINTDIEELPVN	216
		:	
QY	68	FALLTGVGAQVPDHQSIKLSNLGENKH	94
Db	217	SALLQIVGA-----QALKITKILTDLH	238
		:	

```

RESULT 13
US-10-330-773-941
: Sequence 941, Application US/10330773
: Publication No. US20060040262A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
: TITLE OF INVENTION: Novel Compositions and Methods in Cancer
: FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 941
LENGTH: 1552
TYPE: PRT
ORGANISM: Homo sapiens
US-10-330-773-941

```

Query Match	3.3%	Score 208	DB 5	Length 1552
Best Local Similarity	22.0%	Pred. No. 0.00012		
Matches 148	Conservative	82	Mismatches 190	Indels 252
			Gaps	36
Db	572	LNSVQSSPPLTIVPVYPRH-----SENIQFODPRQIQFVEVPRQ-----TGYYPR	621	
Qy	1	MNSQPRQTRSPFPQIQPRPATIENSSPSLR---PQAQIPYAYQANQNHMMYNHLP	56	
Db	622	PPTVPAVAPCVPRFVSNNVPESSLPASMPYADHYSTFSPRRMSSPVQPRPPQRYG	681	
Qy	57	PYPVQGRQYQIQYRHSQ-----PRYVPRPQY-----PVQPRPGCFY	96	
Db	682	PVP--PVPSCMYAVYDSRRIMRPMYQDDIIRSNSLPRMDVHSSVYQTSLEKRYNS	738	
Qy	97	PGPRGDFPMNAYGTPFYPSQ-----PVYQSAPIL--VPRQQ-----	130	
Db	739	LDGYIVACQPPSPERTTVLPREPRCGHLKITSCEQIR-RKPDQAOYHTOKAPVSS-	795	
Qy	131	-----QPP-----PAKRE-----KKTIRIPNPQGGKQITEE-IMSGGQ	163	
Db	796	-----TLPYA--TQSPTRPSPLFSVDFRADPSESQGTFFEDHLSHYMSQGTIGSCIN	849	
Qy	164	SRNPTRPIGRSTSTTPRQQLPSQ--VPEHSPVYGT-VESAHNLAASRPVA-----	212	
Db	850	AIDS-----EPKQVINSNAVLMDLQSGVAKRVRHLPETQRTKEEDPIITPFSQPIIS	903	

Db 213 ASDQKQEKPKDPVLKSPVLRLVLGSEKK-----EQEGQTSHTTAIVSIAELPLRP 266
Qy 904 KKGAISSRSRTGHTTDPVQATASQGSATKPISSVDYVYNADVSRMS-----'----- 952
Db 267 SPTTVSSVARS-----TIAAPTSSALSSQPI-----FTTAIDRCCLSSPREDTIP1 313
Qy 953 ---SYGNEATSSAHYVERRFI-----VTDLSS-HRKHSSGTGDL 988
Db 314 PSTLCTSTSDPLPTNENDDICKPCSVAPNDIPLVSSTNLTNENGVSEKLSATESTV 373
Qy 989 SLELOAKSNSLLQREAN-----ALAMQOKMNSLDEGRHJT 1025
Db 374 ELVKQEVL--PLTLELEINPREMKLEFIVPAATTVSSPSAITYQRLVEE-DESIRTC 430
Qy 1026 LMLLSKEIFELRNGELQSD-YTEDADT-----KP-DR----- 1055
Db 431 LSEDAKEIQ-NKIEVADGQTEIEILDSQNLNSRRSPVPAQIAITVPKTKMKPKDRTRTE 489
Qy 1056 ---DIELELSALDTEPDQSEPIEILIQGLISSQNOQLNGMAVENGHVPQCHQKER 1112
Db 490 EMLEVELELKA-----EBELSIDKVLSESDKMSQGF-----HP---ERDP 527
Qy 1113 PROKKSIGEDH 1124
Db 528 SLLKKVKAIVEN 539

RESULT 14
US-10-840-512-196
; Sequence 196, Application US/10840512
; Publication No. US20050125852A1
; GENERAL INFORMATION:
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: MANNING, GERARD
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: GRIGORIEV, IGOR
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-1455
; CURRENT APPLICATION NUMBER: US/10/840,512
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469,014
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 196
; LENGTH: 2377
; TYPE: PRF
; ORGANISM: Mus musculus
US-10-840-512-196

Query Match 3.3%; Score 207; DB 5; Length 2377;
Best Local Similarity 19.3%; Pred. No. 0.00027;
Matches 216; Conservative 152; Mismatches 424; Indels 326; Gaps 46;
Qy 48 KACPDPQTAINI-----DIDYLPVNALIQVGAQVPRDHQSTKLSNLGEN 92
Db 375 KASPFKSVYIGTPEFMAPMEYBEKYDESVDVYAFGCMLEMATSEXP----- 421
Qy 93 KHYEVAKKCEVDLALYLKPLSGKGVAISNOSAL-----SRPMOKLVTLVN 139
Db 422 -----YSEQNAQAQIYRRTSGVK-PASFDKVAIPVKEKIIISGCIKRONDERYSIDLNL 475
Qy 140 COLVEBEGVYRAMPARASISGERTVTELLIQHONPQOLSNLMAVARCCQFLGPMQOE 199
Db 476 HAFPEBETVAVELAEEDDEGEKAIATLMLRIEDIKLTK-----GKYKDE 520
Qy 200 AKKLVLALDEGSAISKVLVLFVQORLEPRPQAKSTIGHVQ-----LLYRAS 250
Db 521 AIEP-----STDERDVPEDVADQEMVESGYVCBGDKHTAKAIDRVAS 563
Qy 251 CFKVTNRDDSSIMQLKEEFRSYEALRRBHDQIVHIAEAGLRISPEQMSILYGDLLAH 310
Db 564 LTK-RRBEGRQLVREGEKQKQESSFKQONQOASVS-QAGI-----QQLSASASTGIPTA 617

Qy 311 KSHMOSIIDKLOSPESFAKSVQELTIVLQRTDGPANLNRLRPHLELANIDNPDAVSP1 370
Db 618 PATSASVSTOVEPEPEADQHQQ-----LQYQPSISVLS--DGTIDSGQS 662
Qy 371 WEQLENAMAVAKTVVHGLVDPIQNSYRKQHEP-----POPOPNKYKTSMCRD 418
Db 663 SVFTESRVSSQOTVSYG-----SQHEQASHGTAPRGHTVSSIQASQOPHGCVPPSSMAQ 716
Qy 419 LRQGGCCPRGTNCTPAHSGELEKYLRLNKKINATVTRTFPLLN--KGVNNTVTTTAGNV 476
Db 717 GQNGOQ-PSSSLAGVLSQ-----PIQHPOQOQGIQPT----- 747
Qy 477 ISVTSTETTKIVSTNGTISNAENSVSGLISRSTDTLRALETYKVKVKGANGQNAAG 536
Db 748 -----VPSQOAV-----QYSLPQAASS-----BG 767
Qy 537 PSADSVTENKIGSPKTPVSNVAATSAGPSN--VGTELNSVPQKSSPFLTRVPVPPHSE 594
Db 768 TTAQPSQPVQVAGTQPLVQSOTVAIVQSEPHIIPVSTQPSVVVHSGAHLFPMGQPIPTSL 827
Qy 595 NIQYQDPRRTQIPFEVPOY--PQGYPPPTVPAQVACVBRFVRSNNVPSSSLPPASM 652
Db 828 LPQY---PVSQIPRISTPHVSTAQTFSSVPTMAAGING--PLTLASATASSIPGSGSP 882
Qy 653 PYADHYST-FSPRDMNSSPY-----QPPRPQYGPVP-----PVPSG--MYAPVD 696
Db 883 VVBNQLPTLLQPVNLOQSVHPOLLQPTVQSIG-IPANLGOAAREGLPSGVLVYQG-PP 940
Qy 697 SRIWRPPWQORDDIIRNSLPRMDVMHSSVY-QTSLAREVNSLDGYVAVACQPPSEPR1 755
Db 941 SR---LPQYQDPSDINAPSNVASCINHTVLAAPSMPEALATQCYFTTVQPYESTRP 997
Qy 756 TVPLPREPGHLKITSCEQIRKRPQMAQYHTOKAPLVSS-----TL 797
Db 998 IVPW-GSVGQGVQVS-----QPAVSLTQPPPTSSQQAVALVESTQVGAAPPEQT 1046
Qy 798 PVATQSPTRPSPLFS-----VDFRADPSH-----SVSGTFFEDHLSHYSPWSGTIG 845
Db 1047 PITQSQPQPVPLVTSADSAHSDVASGMSDGENAPSSGRHGGRTTKHYNK--SVRS 1103
Qy 846 SCINAIDSEPKDVIAN-----SNAYLMDLSDGVKRVYLFPTQRTKEDEP11PSPDGP 900
Db 1104 RSRHEKTSRPKLRIANVSKGRVYVBCQLETHNKKVYTFKFLDDGNPEFIATIMNDF 1163
Qy 901 IISKGAISRSS-----RTGYHTTDPVQ-----ATASQ 928
Db 1164 IL-----AIERSEFVAQVREIIEKADEMLSEDEVSEPEBGQLESIQKDYGFPGSQKLE 1219
Qy 929 GSATKPISSVDYVYNVAVDSRWSSYGNATSSAHYVERDRTIYDLSGRKHSS---TG 985
Db 1220 GFQKQPIAVSSMPQOIGVPTS-----SLTVVHVSAGR-REIVSVPSRRLRESKVFTS 1271
Qy 986 DELS-LELOAKSNSLLQREBANALAMQOKMNSLDEGR 1022
Db 1272 DISDPVAVASTQAPGMNLSHSASSLQQAPEBLKHGQ 1309

RESULT 15
US-11-096-568A-27756
; Sequence 27756, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27756
; LENGTH: 674
; TYPE: PRF

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM protein - protein search, using sw model

Run on: May 24, 2006, 12:51:45 ; Search time 10 Seconds
(without alignments)
1326.457 Million cell updates/sec

Title: US-10-619-992-2

Perfect score: 6215
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 1113735 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.New:*
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2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB pep.*
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8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	177	2.8	1812	6	US-10-480-434A-14 Sequence 14, Appl
2	171	2.8	577	7	US-11-293-697-3230 Sequence 3929, Ap
3	166.5	2.7	3429	6	US-10-953-349-9275 Sequence 9275, Ap
4	166.5	2.7	3438	6	US-10-953-349-9274 Sequence 9274, Ap
5	166.5	2.7	3478	6	US-10-953-349-9273 Sequence 9273, Ap
6	159.5	2.6	1809	6	US-10-559-415-190 Sequence 190, Appl
7	159.5	2.6	1919	6	US-10-559-415-2 Sequence 2, Appl
8	159	2.6	1057	7	US-11-293-697-3230 Sequence 3230, Ap
9	158.5	2.6	443	6	US-10-953-349-13469 Sequence 13469, A
10	158.5	2.6	451	6	US-10-953-349-13468 Sequence 13468, A
11	158.5	2.6	456	6	US-10-953-349-13467 Sequence 13467, A
12	158	2.5	240	6	US-10-953-349-16346 Sequence 16346, A
13	153	2.5	1384	6	US-10-605-928-799 Sequence 799, App
14	152	2.4	950	7	US-11-293-697-4482 Sequence 4482, Ap
15	151	2.4	343	6	US-10-953-349-21437 Sequence 21437, A
16	148.5	2.4	837	6	US-10-953-349-9736 Sequence 9736, Ap
17	148.5	2.4	846	6	US-10-953-349-9735 Sequence 9735, Ap
18	147.5	2.4	692	6	US-10-953-349-9737 Sequence 9737, Ap
19	145.5	2.3	559	6	US-10-953-349-13784 Sequence 13784, A
20	145.5	2.3	575	6	US-10-953-349-13783 Sequence 13783, A
21	145.5	2.3	598	6	US-10-953-349-13782 Sequence 13782, A
22	144.5	2.3	448	6	US-10-953-349-8748 Sequence 8748, Ap
23	142	2.3	634	7	US-11-293-697-3340 Sequence 3340, Ap
24	140.5	2.3	694	6	US-10-505-928-312 Sequence 312, App
25	140	2.3	295	6	US-10-953-349-23677 Sequence 23677, A

26	140	2.3	849	6	US-10-953-349-1432	Sequence 1432, Ap
27	140	2.3	1003	6	US-10-953-349-1431	Sequence 1431, Ap
28	140	2.3	1392	6	US-10-953-349-1430	Sequence 1430, Ap
29	139.5	2.2	296	6	US-10-953-349-8749	Sequence 8749, Ap
30	139.5	2.2	693	7	US-11-293-697-3849	Sequence 3849, Ap
31	139	2.2	652	6	US-10-953-349-5551	Sequence 5551, Ap
32	138.5	2.2	227	6	US-10-953-349-20011	Sequence 20011, A
33	137.5	2.2	542	6	US-10-953-349-39541	Sequence 39541, A
34	137.5	2.2	592	6	US-10-953-349-39540	Sequence 39540, A
35	137.5	2.2	610	6	US-10-953-349-39539	Sequence 39539, A
36	137	2.2	564	6	US-10-511-937-2557	Sequence 2557, Ap
37	136	2.2	155	6	US-10-953-349-15526	Sequence 15526, A
38	136	2.2	173	6	US-10-953-349-15525	Sequence 15525, A
39	136	2.2	812	7	US-11-293-697-3673	Sequence 3673, Ap
40	136	2.2	4373	7	US-11-118-524-2	Sequence 2, Appl
41	135	2.2	293	6	US-10-953-349-31470	Sequence 31470, A
42	134	2.2	681	6	US-10-953-349-10919	Sequence 10919, A
43	133.5	2.1	454	7	US-11-293-697-3595	Sequence 3595, Ap
44	133	2.1	778	7	US-11-293-697-3043	Sequence 3043, Ap
45	132.5	2.1	161	6	US-10-953-349-18169	Sequence 18169, A

ALIGNMENTS

RESULT 1
US-10-480-434A-14
; Sequence 14, Application US/10480434A
; Publication No. US20060105403A1
; GENERAL INFORMATION:
; APPLICANT: DALIA VENEZIA, NICOLE
; APPLICANT: SIMILINKOVA-ERRARD, OLGA
; TITLE OF INVENTION: BRAIN/ACC ALPHA MOLECULAR COMPLEXES, DIAGNOSTIC AND
; FILE REFERENCE: 0512-1194
; CURRENT APPLICATION NUMBER: US/10/480,434A
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/FR02/02016
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: FR 01/07740
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: FR 02/02789
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
; LENGTH: 1812
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-480-434A-14

Query Match 2.8%; Score 177; DB 6; Length 1812;
Best Local Similarity 18.2%; Pred. No. 0.036;
Matches 232; Conservative 167; Mismatches 470; Indels 406; Gaps 55;

10 EFLSPICYNEDENVHAKISLGCSTHTVCKTLNKLHKK-----ACFPQTAINDIDVL 64
20 KILECPICL-----ELIKEVSTKCDHIFCKFMKLNLNKKGSPQCPLEKNEIT----- 69
65 PNVFALLQVGAQVDPHQSIKLSNGENGVYAKKCVCDLALYLKPLSGGKGVASLNGS 124
70 -----KSLQGSTSPQSLA-----BELLRIMAFELDTGMQLTNGF 105
125 ALSRPWQKLVTLVNCQVVEEGRYVAMRAASLSGRVTEILQHONPOQSLANLMAAV 184
106 SPSKKRN-----SCERLINEASI-----IQSVGRNRRRLQVPER----- 142
185 RARGCOFLPANOEBLKLVLLEDGSLSKKVLVFLVQKLEPRFPQASTSIGHVQ 244
143 -----GNATLKOSL-----GVQLSNLIGIVSKN-----KOTPRKKSIV--YLE 180
245 LLYRASCFVTRRDE-----DSLMLQKEFRFYEALRRHDAQIVHIAEAGLR-ISPQ 299

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Db      181  LDSDSEETVRKGCOSVARDQELLQAPQADGEG--KLHSAEBAACERFSEGRINIEHQ 238
Qy      300  WSSLLYGLAHKSHMOIITDKQSPSPAKSVQELTIVIQRTGDPAANRLAPHELLAN 359
Db      239  CSDDLNPTENHATE-----RHPEK-CQISISINVCPECGTDAHASLIPETSSLL 289
Qy      360  IDPNPDVAVPTWEQLENAMAVAKTVVHGLVDFLOWYSR---KGHETPOPOPSKYKTM 415
Db      230  IEDRNA-----EKAFCNKSQPGIA--VSQSKMAASKGTCNDQVSTGEKV-- 337
Qy      416  CRDLRQGGCGPRGTCTFAHQEELKRYLRNKKINATVTRPPLNKVGNNVTVTAGN 475
Db      338  -----GPN--ADSLDERKW-----THP--QSLCPENSGATTDPV 368
Qy      476  VTSVIGSTE-----TGKIVPTNGI-----SNAENSVSOLISSTSTILAEITVK 523
Db      369  WITLNSVQKVNEMWFSRTGEMLTSDSARHESNAEAALVLEVSNEVDG--GESSRK 425
Qy      524  VGVKVG-----ANGQNAAGPSADSVTENKIGSPPTKPVSNVATSAAGPNSVGTLS 574
Db      426  TDLVTPDPHHTLMCKSGRDFSKFVEINISDKIFGKSYQKSGR-----PHLH 473
Qy      575  VPQKSSPILT--RVVYPPHSENIQYFODPTQIPEVPQYQYPPPTVPAG--V 629
Db      474  VTEIGTFITEPQIQEQPFTWKLKRRGTSIQEDFIKKADAGVQRTPDNINOCTDIM 533
Qy      630  AACVRFVANSNVPESSLPPASMPYADHSTFSPRNMSSPYQPPPPQYGVPPVPSG 689
Db      534  ENEQAVSTTSCQEKKIASNL--QKESKAHPESLKEP-----572
Qy      690  MYAPYDSRRIRMPWYQRDIIIRNSLPPMDV--MHSSVYQTSLEERYNSLDGYSA 746
Db      573  --ASTAGAKSI-----SNVSDDLVEALNHVSHSKAKRRLKRS-----SIR 612
Qy      747  COPSEPRITVPLPREPCGHLKT---SCEEOIRRRPDQMAOYHQKAPLVSTLPAQ 802
Db      613  CALPLEPIRNPSP--PTCAELQIDSCGSEETKKNHNOQPAHLREPOLIEDTEPAADA 671
Qy      803  SPTPSPPLFSVDFRADFSSESGTKEEDHLSHYWSGCTIGSCINADSEPKYDIANS 862
Db      672  KNEPN-----BHRRK-----RAADAPFEELKMK 697
Qy      863  NAVLMDLSDGVKRVHLFETQRTKEBDPIIFPDGPIISKGAISRSGTYHTTDPV 922
Db      698  AGLLTSCSS-----PKSGQPVN-----SFQRTTQBLER 729
Qy      923  QATAS-----QGSATKPIVSVDYVYNAVDSRMSSYGENEATSSAHYERDR 969
Db      730  QMSDSAKELGDRVLGEPGKTTDRSEESTSVLSV--DTDYDTQNSVGLDAHTV---- 783
Qy      970  FIVTDLSGRKHSSTDDLSLEQAKNSLLQREANALMAQKNSLDEG-----RHL 1024
Db      784  -----RYARTSACQCTQFVASENPKELMHGNS--NAGSGTEGAKPLRH- 826
Qy      1025  TINIISKEIERNGELOSPTYE-----DATDTPKDRDIEELS 1062
Db      827  ALNLSQEKEMBESELDIOTLQNTFOVSKQSFALFSKRSRPOKCAHVSPELSKPKYT 886
Qy      1063  ALDTD--EPDQSEPIEILDIQ-----LGISQNDOLINGNAVENGHV--QOHQKEP 1112
Db      887  AKGKQKQEQOE--FEISHVQAVATVGLPVCQCGKLADMTMCRGCLCSSHYRS- 943
Qy      1113  PKQKQSLGEBDHYILEQKTIIPVTSQFQGPLVSIASNSCLPITTSVSAQNILKTHW 1172
Db      944  -----BENG--LSATGSGISQNSHFQ-----SVSPIRSSI----- 973
Qy      1173  SEDKNDLKPVANGK 1187
Db      974  ---KTDNRKPLETGR 985

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RESULT 2

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US-11-293-697-3929
; Sequence 3929, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3929
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3929

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Query Match      2.8%; Score 171; DB 7; Length 577;
Best local Similarity 22.0%; Pred. No. 0.016;
Matches 98; Conservative 50; Mismatches 147; Indels 150; Gaps 20;

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Qy      511  TSTLRALETYKVGKVGANGQNAAGPSADSVTENKIGSPKTPVSNVATSAAGPNSVGT 570
Db      51  KTSLSLPYHT-----SSTHPEVTPRTYTNITPKHTGTGRTPVAN--TTASASSRLPT 102
Qy      571  EL--NSVPQKSSPFLTRVNV-----YPPHSENIQYFODPTQIPEVPQY----- 613
Db      103  PFTTHSPFGSSPFGSTGWTATSPQTTTYTTPSH-----PQTLPTHVPFSTSLV 155
Qy      614  -----POTGYPPPTVPA-----627
Db      156  TPTHTVITITHTQMATASISHTPTGTVPPPTLTKATGSTHTAPMTVTTSGTSHSS 215
Qy      628  GVAQVPRFVNSN--VPE--SSLPPAS-----MPADHYSTFSPDRMNSPYOPPPQ 678
Db      216  FSTATASSFISSSWLPONSSSRPSSPRTYQPLUSSATTIVSTTNOLSFSSPSA 275
Qy      679  PYGVPVPSGMYAPYDERRIWRPWOYRBDIIRNSSLPPMDVMSVYQTSLEERYNS 738
Db      276  PSTVSVVPSHSSPQTS-----PSVGRSSFV--SAP-----VASTLSSGSHSLST 323
Qy      739  LDGYSVACQ--PSEP-----RTTVPLPREPCGHLKTSCEQIRKRPDQMAQYHTQX 790
Db      324  HPTTASVSASPLFPSSPAASTTIRATLP-----HTISS 356
Qy      791  PL-VSSTLPA--TOSPTPSPPLFS 812
Db      357  PFTLSALPLISTVTVSPSPSHLAS 381

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RESULT 3

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US-10-953-349-9275
; Sequence 9275, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9275
; LENGTH: 3425
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana

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US-10-953-349-9275

Query Match 2.7%; Score 166.5; DB 6; Length 3429;
Best Local Similarity 19.2%; Pred. No. 0.33;
Matches 219; Conservative 151; Mismatches 439; Indels 331; Gaps 53;

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QY 307 DLAKH-SHMOIITDKLOSPESF-----AKSVQELTIVLQRT----- 341
DB 1248 PGSDSFAHIPSIRLVETDDKLLEYTKLNDVPVNAKESTVGMRKQSGMGLDTHQY 1307
QY 342 GDPANILNRLRPHLELLANID-----PNPDVSPTEQOLENANVAVKTVHGLVDFIQ 394
DB 1308 GKGKRAEVRYSYEKLTBEFEKLCQTESPDSPQKGSESSSLANDTSNIP-----VEN 1362
QY 395 YSRKGHEPQP-QPNSKYKTSMCRLDROGGCPRGNTCTFAHQEELKYLKKNKINAT 453
DB 1363 SS-----DTLLPSPQAITVQPMEPVRPQ-----SHTLKEETOPIKKGRGRPK----- 1406
QY 454 VTFPPLNKVGNNTVTTTA-GNVISVIGSTETTKIVPSTNGISNAENSVSOLISRTD 512
DB 1407 -RTDKALTPVSLSAVSRTQATGNAIS---SAATGLDFVSDKRLAASHPTSLSALTSPD 1462
QY 513 -----STLRALETYKVKVKGANGQNAAG---PSADSVTENKIGSPPKT 553
DB 1463 LSGPFGFQSLPASPAFTPIRGGRGRSGRGAAGRVRGVLHGNSISITQR----- 1514
QY 554 PVSNNVAATAGSPNVTGLNSVPQKSPFLTRVP-----VYPPHS----- 593
DB 1515 ---TETATSLASDAETKFE-ALPRASASEIVSRVPKNEGSTNPDQVSHSATTALRS 1570
QY 594 -----ENIQYFODPRTQIPEFYQYR-----QGYVPPPTVP----- 626
DB 1571 KAADKDLAPPGFDGSHVQTLNVLNLSSEBRKAFVKKRPLIQGVSSQHPGPKQPLDLP 1630
QY 627 -----AGVACPVPFVRSNNVPBESSLPASMPY-ADHYSTFSPDR---MNSSPYQ-- 673
DB 1631 VSTSTSLGGGVQONAVSVCDGSKSPSEGRITYALQGVTTAPDATALPMSQGS DAT 1690
QY 674 -PPPOPYGP-----VPPVSGMYAVYDSRRIRWRPMPY---QRDDIIRNSLPPM 720
DB 1691 LPMSSQPVGSTVEAOEANVPSPALPA---KRRVRNLPBSRGETPKRQKRGKGOPLPAT 1746
QY 721 DVMSHSSVQTSI---RERYNSLIDG---YGSVACQPSSEPTTVLPREPCHLKTSGE 772
DB 1747 DA--SSASTGTLPTQIEVKVGNLSGTAKAFDAVAKEQPHFSQVA---PDHSSGSLS 1799
QY 773 BOIRR-----KPDQWAOYHTOKAPLVSSTLPVATOSPPTPSP- 809
DB 1800 QGIRBDTSGTGSARKQOTADVTVAVKMEIFSETSLKHKVGEPATRTTNVPDAQSPG 1859
QY 810 ---LSVDRADPSESVSCTFEE-----DHLSHYSPMCCGTTGSCINADSE 854
DB 1860 EMNLHIVETHTK--ABDSSGLKQOEALYNLSKADKLVSDIPHPVPGDLTSSGSVAN----- 1912
QY 855 PPOVANSNAV-----LMDLSDGVKRRV---HLFET-----QRTKTEE 890
DB 1913 -KVDIGSSKVAENELVKIPGADVDSVYQUSLGLTTLAKSSLEKCTADQLGKLSQE 1971
QY 891 DRIIPESDPIISKMGAISSRSTGYHTTDPVQATISQGSATKPIVSVDVPPYNAVDSR 950
DB 1972 GETTPASDETCHL--AEETASLSYVRSP---TASASTTAEPRLPTDLKKNISFODE- 2025
QY 951 WSSYGNHATSSAHYVRDRFIYTDLSGHRKHSSTGLLSLELOAASNSLLOREANALA 1010
DB 2026 -----VKTLLGDKREAL---LLSSE--EOTVNSKIX---ETNSSE 2057
QY 1011 MOOKNMSLDEGRHLLNLNLKSEITELANGELOSDYTEDATDTKPDRIELELSALDDEPD 1070
DB 2058 LQA---SRTEBVRHVD---GKSVYDANQVYKED-----EAKHSVEIQQSSMLERDELDP 2103
```

```
QY 1071 GQSEPIEETLIDQ-LGISSQNDQLNGMAVENGHPVQOHQKPEPKOKKOSLGEDHYILE 1129
DB 2104 NAGQGHSSIIDQPIVLYTISNE---NAMSILD-----KQYDPIRSKADIDQ----- 2147
QY 1130 QKTLIPVTSFQSPPLPVSTISNASCPLITTSVAGN---LILKTVWSEEDKNDFLKFPVANG 1186
DB 2148 -----PEESVFQV---GVGRPKVGTADTQMEDTNDAKLLVGCSSVSESEKTKLQSLTIG 2198
```

RESULT 4

```
US-10-953-349-9274
; Sequence 9274, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 9274
; LENGTH: 3438
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9274
```

Query Match 2.7%; Score 166.5; DB 6; Length 3438;
Best Local Similarity 19.2%; Pred. No. 0.33;
Matches 219; Conservative 151; Mismatches 439; Indels 331; Gaps 53;

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QY 247 YASCFKTKRDESSLMQKEEFRSYEARREHDAQIYHIMEAGLRISPEOWSLLYG 306
DB 1199 YLESILRESKKEEDAPV--LDDDALNDLIARRESEIDIFESIDKOKENEMETWNTLVHG 1256
QY 307 DLAKH-SHMOIITDKLOSPESF-----AKSVQELTIVLQRT----- 341
DB 1257 PGSDSFAHIPSIRLVETDDKLLEYTKLNDVPVNAKESTVGMRKQSGMGLDTHQY 1316
QY 342 GDPANILNRLRPHLELLANID-----PNPDVSPTEQOLENANVAVKTVHGLVDFIQ 394
DB 1317 GKGKRAEVRYSYEKLTBEFEKLCQTESPDSPQKGSESSSLANDTSNIP-----VEN 1371
QY 395 YSRKGHEPQP-QPNSKYKTSMCRLDROGGCPRGNTCTFAHQEELKYLKKNKINAT 453
DB 1372 SS-----DTLLPSPQAITVQPMEPVRPQ-----SHTLKEETOPIKKGRGRPK----- 1415
QY 454 VTFPPLNKVGNNTVTTTA-GNVISVIGSTETTKIVPSTNGISNAENSVSOLISRTD 512
DB 1416 -RTDKALTPVSLSAVSRTQATGNAIS---SAATGLDFVSDKRLAASHPTSLSALTSPD 1471
QY 513 -----STLRALETYKVKVKGANGQNAAG---PSADSVTENKIGSPPKT 553
DB 1472 LSGPFGFQSLPASPAFTPIRGGRGRSGRGAAGRVRGVLHGNSISITQR----- 1523
QY 554 PVSNNVAATAGSPNVTGLNSVPQKSPFLTRVP-----VYPPHS----- 593
DB 1524 ---TETATSLASDAETKFE-ALPRASASEIVSRVPKNEGSTNPDQVSHSATTALRS 1579
QY 594 -----ENIQYFODPRTQIPEFYQYR-----QGYVPPPTVP----- 626
DB 1580 KAADKDLAPPGFDGSHVQTLNVLNLSSEBRKAFVKKRPLIQGVSSQHPGPKQPLDLP 1639
QY 627 -----AGVACPVPFVRSNNVPBESSLPASMPY-ADHYSTFSPDR---MNSSPYQ-- 673
DB 1640 VSTSTSLGGGVQONAVSVCDGSKSPSEGRITYALQGVTTAPDATALPMSQGS DAT 1699
QY 674 -PPPOPYGP-----VPPVSGMYAVYDSRRIRWRPMPY---QRDDIIRNSLPPM 720
DB 1700 LPMSSQPVGSTVEAOEANVPSPALPA---KRRVRNLPBSRGETPKRQKRGKGOPLPAT 1755
```

```

Qy 721 DVMSHVVYQTSI-----RERYNSLDG-----YYSVACOPSEPRTPVPLPREPCGHLKTSCE 772
Db 1756 DA--SSASTGLTLPQIEVKVGNLSGTAKAFDAVAEQPHFSQSA-----PIHSSGSLIS 1808
Qy 773 EOIRR-----KPDQMAQYHTQAKAPLVSSSTLPAVATOSPPTPSP 809
Db 1809 QEIRRDTSGTGSAARKQTADVTVARVMKEIFSETSLKHKGGEPSATRTTVPPAQSFG 1868
Qy 810 ---LFSVDFRADFSHVSSTGTFEE-----DHLSHSPMSCGIGICINAIQSE 854
Db 1869 EMLHTVETHK--AEDSSGLKNQOEALYNLSKADKLVSDFPHFPGDGLTSSGVAN----- 1921
Qy 855 PKDVANSNAV-----LMDLDSGDYKRRY--HLFET-----QRTKEE 890
Db 1922 -KDVIGSSKVAANEELVKI PGGDVDSVYQLSLGNTLLTAKSLSEKCTADQLLGEKLSQE 1980
Qy 891 DPILPSPGPIISKMGALSRSSRTGHTTDPVOATASQGSATKPIVSVDYVYVNAVDSR 950
Db 1981 GETTPASDGETCHL--AEETAASLSYVSEF--TASATTAEPLEPTDLKKNISFQDE- 2034
Qy 951 MSSYGNEMATSSAHYVERDRFIYTDLSGHRKHSSTGDLISLEIQAKNSLLLOREANALA 1010
Db 2035 -----VKTUNGDKRRAI--LSSSE-EQTNVNSKI--ETNSSE 2066
Qy 1011 MOOKMNSLDEGRHLTLNLSKEIERNGELOSDYTEDATDTKPRDIELELSALDTPDEP 1070
Db 2067 LQA--SRDDEVPHVD---GKSVVANQTVKED-----EAKSVLEIQSMLEPDEL 2112
Qy 1071 GQSEPIEELDIQ-LGISSQNDQLNGAVENGHPVOHQKPEPKOKKOSLGEDHYILEE 1129
Db 2113 NAGQGHSSIDQLPVLVYTSNE--NAMSGLD-----KQYDPIFSKADIBOD----- 2156
Qy 1130 QKTLIPVTSCEFSQPLPVISINASCPIITTSVAGN---LILKTHVMSSEKNDPLKRVANG 1186
Db 2157 -----PEESVFVQ---GVGRPKVGTADTQMEDTNDAKLLVGCVSSESEKEXTLOSILPG 2207

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RESULT 5

```

US-10-953-349-9273
; Sequence 9273; Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 9273
; LENGTH: 3478
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9273

```

Query Match 2.7%; Score 166.5; DB 6; Length 3478;

Beet Local Similarity 19.2%; Pred. No. 0.34; Indels 331; Gaps 53;

Matches 219; Conservative 151; Mismatches 439;

```

Qy 247 YRASFCKYTKRDESSLMQKEFRSYEARLRERHDAQIVHIAEAGLRISPRQWSSLLVG 306
Db 1239 YLESILRESKKEEDAV--LDDDALNDLILARRSEIDIPESIDQKQENEMEMTWTLVHG 1296
Qy 307 DLAHK-SHMOSIIDLKQSPESF-----AKSVQELTIVLQRT----- 341
Db 1297 PDSDFAHIPISIPSRVLVTEDDLKLLEYTKLNDVPMVAKESTVGMKRGKSGMGLDTHQY 1356
Qy 342 GDPANLNRIRPHLEILANID-----PNPDAYSPTMEOLENANAVKTVVGLVDVFION 394
Db 1357 GKGKARAREVRSYERKLTSEEFELCTQTESPDSFGQGBGSESSLANDTSNIP-----VEN 1411
Qy 395 YSRKGHETPOP-QPNASKYKTSMCRDLRQGGCGPRGTNCTFAHSQEBLEKYLKNNKKNAT 453

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Db 1412 SS-----DTLLPFTSPTQALITVQPMEEVRPQ-----SHTLKEETQPIKRGRRPK----- 1455
Qy 454 VRTPELKLKGVNNVITTTA-GNIVSVIGSTETTCIKIPSTINGISNANNSVQSLISRSND 512
Db 1456 -RTDKALTPVSLSAVSRTQATGNALIS--SAATGIDPFSSDKRLPAHSPTSLMLTSD 1511
Qy 513 -----STLRALLETVKVKGAVQANQANAG--PSADSTENKIGS PPKT 553
Db 1512 LSGPRGFSQSLPASAPPTIRGGRGRSRGRGARRVGEVLHGNSNSITQ----- 1563
Qy 554 PVSNTVAATSGPSNVGTSLNSVPQKSPPLTRVP-----VYPPHS----- 593
Db 1564 ---TETATSLASDAEATKF-ALPRGASEIVSRVPRPANGSTSNPDQVSPVHSATTALRS 1619
Qy 594 -----ENIQYFQDRRTQYPFVVPQY-----QNGYVPEPTVP----- 626
Db 1620 KAADKDLAPGFGDSGHVQTLNLVNSSERKAFVKKRPLIQVSSQHPGNKQPLDL 1679
Qy 627 -----AGVAPCVPRFVRSNNVPESSLPASMPY-ADHYSTFSPDR--MNSSPYQ-- 673
Db 1680 VSTSTLLGCGFVQONQNAVSSVCDGSKSPSEGRITTLAQVTTAPSDATLPMSSQPSAT 1739
Qy 674 -PPPOPYGP-----VPPVSGMYAPVYDSRIWPRPMY-----QRDDITRNSLPM 720
Db 1740 LPMSSQPVGSTVEAOEAVNPSPILPALPA---KREVRNLPKGETPKRGKRRGQPLPAT 1795
Qy 721 DVMSHVVYQTSI-----RERYNSLDG-----YYSVACOPSEPRTPVPLPREPCGHLKTSCE 772
Db 1796 DA--SSASTGLTLPQIEVKVGNLSGTAKAFDAVAEQPHFSQSA-----PIHSSGSLIS 1848
Qy 773 EOIRR-----KPDQMAQYHTQAKAPLVSSSTLPAVATOSPPTPSP 809
Db 1849 QEIRRDTSGTGSAARKQTADVTVARVMKEIFSETSLKHKGGEPSATRTTVPPAQSFG 1908
Qy 810 ---LFSVDFRADFSHVSSTGTFEE-----DHLSHSPMSCGIGICINAIQSE 854
Db 1909 EMLHTVETHK--AEDSSGLKNQOEALYNLSKADKLVSDFPHFPGDGLTSSGVAN----- 1961
Qy 855 PKDVANSNAV-----LMDLDSGDYKRRY--HLFET-----QRTKEE 890
Db 1962 -KDVIGSSKVAANEELVKI PGGDVDSVYQLSLGNTLLTAKSLSEKCTADQLLGEKLSQE 2020
Qy 891 DPILPSPGPIISKMGALSRSSRTGHTTDPVOATASQGSATKPIVSVDYVYVNAVDSR 950
Db 2021 GETTPASDGETCHL--AEETAASLSYVSEF--TASATTAEPLEPTDLKKNISFQDE- 2074
Qy 951 MSSYGNEMATSSAHYVERDRFIYTDLSGHRKHSSTGDLISLEIQAKNSLLLOREANALA 1010
Db 2075 -----VKTUNGDKRRAI--LSSSE-EQTNVNSKI--ETNSSE 2106
Qy 1011 MOOKMNSLDEGRHLTLNLSKEIERNGELOSDYTEDATDTKPRDIELELSALDTPDEP 1070
Db 2107 LQA--SRDDEVPHVD---GKSVVANQTVKED-----EAKSVLEIQSMLEPDEL 2152
Qy 1071 GQSEPIEELDIQ-LGISSQNDQLNGAVENGHPVOHQKPEPKOKKOSLGEDHYILEE 1129
Db 2153 NAGQGHSSIDQLPVLVYTSNE--NAMSGLD-----KQYDPIFSKADIBOD----- 2196
Qy 1130 QKTLIPVTSCEFSQPLPVISINASCPIITTSVAGN---LILKTHVMSSEKNDPLKRVANG 1186
Db 2197 -----PEESVFVQ---GVGRPKVGTADTQMEDTNDAKLLVGCVSSESEKEXTLOSILPG 2247

```

RESULT 6

```

US-10-559-415-190
; Sequence 190; Application US/10559415
; Publication No. US20060100132A1
; GENERAL INFORMATION:
; APPLICANT: Astrazeneca AB et al
; TITLE OF INVENTION: Diagnostic Method
; FILE REFERENCE: 101073-1P WO
; CURRENT APPLICATION NUMBER: US/10/559,415

```

CURRENT FILING DATE: 2005-12-06
 PRIOR APPLICATION NUMBER: 0313081.2
 PRIOR FILING DATE: 2003-06-06
 NUMBER OF SEQ ID NOS: 191
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 190
 LENGTH: 1809
 TYPE: PRT
 ORGANISM: Homo Sapiens - peptide sequence of amino acids
 US-10-559-415-190

Query Match 2.6%; Score 159.5; DB 6; Length 1809;
 Best Local Similarity 19.1%; Pred. No. 0.33;
 Matches 246; Conservative 174; Mismatches 429; Indels 437; Gaps 66;

```

QY 48 KACPDDQAININDIVLPVNFALLQLVGAQVDPHOSIKLSNGENHGYVAKKCVEDLAL 107
DB 351 KSTSEKKAANEEMAL-----RQIKD--TVTMADAGRANKEVEILRKQCALCO 397
QY 108 YKPLSGGKVASLNS-----ALSRPMQRKLVTLVNCQVVEEGRVRA--RA 154
DB 398 ELKEALQEADVAKCRDMAFOERDKIVARSDIRTL-----CDNLRR--RDRAVSELARA 451
QY 155 ARSLGE-----RTVELILQHONPOOLSANLMAVARAGCQFLGPMOBEALKVLV 205
DB 452 LSLSDTRKQKNDVRELKEL-----KQMESQLEKEARFR--QLMAHSHDSALDIDS 503
QY 206 LALE-----DGSALSRKVLVLFVYQRL--EPRFPQ-----ASKTSIGHVVQLVYRASC 251
DB 504 MEMETEVEFERETEDIDIKALGFDMAGVNEPCFGDCGIFVTYKDKGSINDGRLRVND 563
QY 252 FYVTRKDESSLMOLKEERSEYAL-----RREHDAQIV--HIAM---EA 291
DB 564 WLIRINDV--LINDKKQALKALINGGAINMVRRRKSLGKVVTLPHINLSGQKXS 620
QY 292 GLRISPEQW--SSLYXDGLAKHSMOSIIDLQSPESFA---KSVQELTIVLQRTGDPANL 347
DB 621 GISTLENGVAAAVLPSSPAKESGLAVGRIVAINIADNKSLSNCESLRKCQDSLTL 680
QY 348 NLRPLHELLELANIDPNDAVSPTEQOLENAMAVALKTVHGLVDLFIONYSRKGHETPOPOP 407
DB 681 SILK-----VFPQ-----SSSW-----SGQNIFFENIKQSDKMLSFRAH--GREVOA 719
QY 408 NSK-----YKTSMCRDLRQGGCPRGNTCTPASPQELERKRLRNKINAT 453
DB 720 HKRRLIOHNNSTQTDIFYTDLERKEG--PPGSSSFLH----- 759
QY 454 VRTFPLNKVGNNTVTAGNAVIVISGSETTGKIVPSTNGISNAENGSQLISRSTDS 513
DB 760 -KPPF-----GGFLQVCPOACPSA-----SERLSFRSDASGD 792
QY 514 TLRALETYK-----KVGKVGANQONAGAPSDVSTENKIGSPKPTPVSNVAATSA 563
DB 793 RGFGLVDVGRRLPLPFETEVGPGCVG--EASLDKADSGSNCGTWPFLAMLSSTA----- 846
QY 564 GGSNNGTELSNPQKSSPFLTRVVPVPPHSENIQYQDPRTOIPEFVPOY--POTGY----- 618
DB 847 -----VPEKLS-----YKKKPKORSIF--DENT--FKRPQTPPKIDILPG 884
QY 619 -----YPPPTVPAG--VAPCVPRFVNSNV-----PESSUP 648
DB 885 PGPAPSPQSKAGAPLTPPKPRR--RSDSIKFOHRLTSSSEBATTLVGSSPSTSPSALP 942
QY 649 P-----ASNRYADHYSTFSP-----RDR 666
DB 943 PVDVGEPMHAGPPRKARVRIASSYYPEDGDSHLPAKKSCEDELTSQKVDDELQKRRR 1002
QY 667 MNSSP--YQP-----PPQPYGPPVPSPGMYAPVYNSRRI 700
DB 1003 PKSASBFRKLAPVVIIPAQLEBQKVPASGELISFLQEMAP-----YSGHSHRS 1054
QY 701 WRPPMYORDIIRNSLPRMDVHSSVYQTSLRERNYSLDGYYSVACQPPSEBRTVPLP 760

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DB 1055 -NPPLYPSR-----SVGTVPRLSTPTTSG$ILRNPIYTVRSHRVGCPSSPAPADAGPQG 1110
QY 761 REPCHLTKTSCBEOIRKRPD-----QMAQYHTQKAPLVSSTLVPATQSPRPSPSLFVSDPR 816
DB 1111 LHP-----SVOHQGLSLDLSHRITCSDYSEMRATGNSLPSASRLGSSS-----NLOFK 1160
QY 817 AD-----PSESVSGTKFEEDHLSH-----YSPWSCGIGSCINADISE-----PKD 857
DB 1161 AERIKIPSTPRYPRSVYGS--ERGSVSHSECSTPPQSPPLNIDTLLSCSOSQTSASLPLR- 1217
QY 858 VIANSNAVLMDDSGDVKRRVHLFETQRTKEEDPIIPF-----SDQPIISKWGAIS 909
DB 1218 -IANNPAST-----GRRRDRPYVEEPRHVKYQKXSEPLGISIVSEKGGIYVSKTVGS 1271
QY 910 RSRRTGYHTTDPV-----QATASQ-----GSATKPIYV--SDVPPYVNAVDSRWSSY 954
DB 1272 IAHQAGLEVGDOLLEENGINLRSAEQARLLIGQCCDPTITLTAQYNPHVHOLS----- 1326
QY 955 GNEATSSAHYVERDRITVTDLSGHR--KHSTGDLISLELOQ-----AKSNGLLQREA 1006
DB 1327 --HSRSSHLDPAGTHSTLQSGGTTTPHPSPVIDPL--MEQDEGPTPPAKQSSSRLAGDA 1383
QY 1007 NALAMQO-----KMSLDEGRHLTLNLSKEIELRNGELQSDYTEDATDTKPPDR----- 1055
DB 1384 NKKTLEPRVVFIRKQGLEIGHVLC-----CGNLHGVAVEVEDSPAKGPDGLV 1432
QY 1056 --DIELESLADTDEPDGQSEPIEET 1079
DB 1433 PGDLILEYGLSDV-----RNKTVEEV 1453

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RESULT 7

US-10-559-415-2
 ; Sequence 2, Application US/10559415
 ; Publication No. US20060100132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Astrazeneca AB et al
 ; TITLE OF INVENTION: Diagnostic Method
 ; FILE REFERENCE: 101073-1P WO
 ; CURRENT APPLICATION NUMBER: US/10/559,415
 ; CURRENT FILING DATE: 2005-12-06
 ; PRIOR APPLICATION NUMBER: 0313081.2
 ; PRIOR FILING DATE: 2003-06-06
 ; NUMBER OF SEQ ID NOS: 191
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2
 ; LENGTH: 1919
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-559-415-2

Query Match 2.6%; Score 159.5; DB 6; Length 1919;
 Best Local Similarity 19.1%; Pred. No. 0.36;
 Matches 246; Conservative 174; Mismatches 429; Indels 437; Gaps 66;

```

QY 48 KACPDDQAININDIVLPVNFALLQLVGAQVDPHOSIKLSNGENHGYVAKKCVEDLAL 107
DB 461 KSTSEKKAANEEMAL-----RQIKD--TVTMADAGRANKEVEILRKQCALCO 507
QY 108 YKPLSGGKVASLNS-----ALSRPMQRKLVTLVNCQVVEEGRVRA--RA 154
DB 508 ELKEALQEADVAKCRDMAFOERDKIVARSDIRTL-----CDNLRR--RDRAVSELARA 561
QY 155 ARSLGE-----RTVELILQHONPOOLSANLMAVARAGCQFLGPMOBEALKVLV 205
DB 562 LSLSDTRKQKNDVRELKEL-----KQMESQLEKEARFR--QLMAHSHDSALDIDS 613
QY 206 LALE-----DGSALSRKVLVLFVYQRL--EPRFPQ-----ASKTSIGHVVQLVYRASC 251
DB 614 MEMETEVEFERETEDIDIKALGFDMAGVNEPCFGDCGIFVTYKDKGSINDGRLRVND 673
QY 252 FYVTRKDESSLMOLKEERSEYAL-----RREHDAQIV--HIAM---EA 291

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Db 674 WLLRINDV---LINKDKQAIIKALINGEGAINMVRRRKSLGKVTPPLHINLSGQKXS 730
QY 292 GLRISPEQW--SSLYGLDLAKHSMQSIIDKQSPESFA---KSVQELTIVLORTDPPNL 347
Db 731 G1SLBNGYAAAVNLQSSPAKSGSLAVGRIVANGIALDNKSLBCECSLSCQDSLT 790
QY 348 NLRPLHLEILANIIDNPDAVSPTEWOLEENAMAVAVTVVHGLVDVFIQNSRKQHETPOPOP 407
Db 791 SILK-----VFPQ-----SSSW-----SGQNFENIIDSQKMSLFRAH--GREVOA 829
QY 408 NSK-----YKSMCRDLRQGGCGPRGNTCTFASQEBLEKYLRLNKKINAT 453
Db 830 HMKRMUOHNNSTQDIFDYTLDELRKEBG--PPGSSSFFLH----- 869
QY 454 VTFPLKLVGVNNVTTAGNVISIGTERTGKIVPTNGISNAENVSQILSRSTDS 513
Db 870 -KPPF-----GGPLQVCPQACPSA-----SENSLSFRSDASD 902
QY 514 TLRALETVK-----KVGKVGAMGQNAAGPSADSVTENKIGSPKTPVSNVAATSA 563
Db 903 RQFGLVDVGRRRPLPFETEVGPCVG--EASLDKADSGNSGGTWPKAMLSSTA----- 956
QY 564 GBSNVGTBLNSVPQKSSPFLTVPVYPPHSENIQYFQDPRTOI PREVPQY--POTGY---- 618
Db 957 -----VPEKLS-----YKKEPKOKSKIF-DEMT--FKRPQTPEKIDYLLPG 994
QY 619 ---YPPPTVAG--VAPCVPRVRSNNV-----PRESSLP 648
Db 995 PGPAAHPOPSKRAQGLTPPKPR--RSDIKFOHRLTSSBEBATLVGSSPSTSPSALP 1052
QY 649 P-----ASNRYADHYSTESP-----RDR 666
Db 1053 PVDVGPBPMHASPRAKARVRIASSYVPEGDGSHPFAKSCDEDLTQKVDLQKRRR 1112
QY 667 MNSSP-YQP-----PPQYGVPPRPVPSGMAYAVYNSRI 700
Db 1113 PKSASFSRKLAPVYI PAQFLBEOKCVPASGELSPLQEMAP-----YSGHSSRHS 1164
QY 701 WRPWQORDIIRSNLSLPRMDVMHSSVQTSLRERNNSLDGYVAVACQPPSEPRTPVPP 760
Db 1165 -NPPLYPSP--SVGTVPRLSTPTTVSILBNPITYVRSRHRVGCSSPPAPARADPQG 1220
QY 761 RPPCGHLKTSCEBQIRKRPD---QMAQYHTOKAPLVSTLPVATQSPTPPSPFSVDR 816
Db 1221 LHP-----SVQHQRSLSLDLSHRTCSQVSEMKRATGNSNLSPSARLSSS---NLQPK 1270
QY 817 AD-----FSESYSGTKFEEDHLSH-----YSPMSCGTIGSCINAIDSE---PKD 857
Db 1271 AERIKIPSTPRYPRSVVGS--ERGSVSHSECSSTPPQSPPLNIDTLLSSCOSQTSASTLPR- 1327
QY 856 VIANSAVAMDLDGQDVKRHLFETQRTKEEDPIIFP-----SDGPIISKGAIS 909
Db 1328 -IAVNPASL-----GERRKDRPVVEPRVAVKQKSEPIGISTVSEKKGIVYKATVGS 1381
QY 910 RSSRTGYHTTDPV-----QATASQ-----GSATKPIV--SDVPRVYNAVDSRMSY 954
Db 1382 IAHQGLEXYGDOLLENGINLSATQEQARLIIGQCCDTITLIAQNPVHQSS----- 1436
QY 955 GNEATSSAHYVERDRITVLDLSGR--KISSTDLLSLEIQ-----AKSNLLIQRRA 1006
Db 1437 --HSRSSSHLDPAQTHSTLQSGSTTPTEHPHSVIDPL--MEQDEGSPSTPPAKQSSRIAGA 1493
QY 1007 NALAMQO-----KMSNLDEGRHLLNLKSEILRNGELQSDYTEDATQTKPR----- 1055
Db 1494 NKKTEPRVVFYTKSQLELGVHLC-----GNNLHVAVAEVEDSPAKGPDGLV 1542
QY 1056 --DIELESLALDTEBPQSGSEPIEET 1079
Db 1543 PGDLILEYGLDY-----KNKTVEEV 1563

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RESULT 8
US-11-293-697-3230

```

; Sequence 3230, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 3230
; LENGTH: 1057
; TYPE: PR
; ORGANISM: Homo sapiens
US-11-293-697-3230

```

Query Match 2.6%; Score 159; DB 7; Length 1057;
Best Local Similarity 19.6%; Pred. No. 0.17;
Matches 146; Conservative 100; Mismatches 264; Indels 234; Gaps 36;

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QY 554 PVSNTVAATSA-----GPSNVGTBLNS-----V 575
Db 3 PARSVASTSAXNDLNLRSQTKDCHLRHFVDVPLNLOQRPPOETGERLNKYEHRRI 62
QY 576 PQKS---SPFLTRVPVPPHSENIQYF---ODPRTOI-----PFEVP 611
Db 63 LOESIDVAFPTTKIKIGLEBERENYSRVASSSSPKSHIITKOMDVRSVSDLYKMGHSVP 122
QY 612 Q-YPOTGYVPPPTVAGVAPCVPRVRSNNVPESSLPPASNP-----YADHYSTESP 663
Db 123 QSLPQSNVPT-----TLNSVYVNE--PPRSYPSKEVSNLYGKQSNAL 164
QY 664 RDRMN-----SSPYQPP--POPYGVPRVPSGMAYP-----YDSRRIRWRPM 705
Db 165 AAAAPQITLSTITSLSKRPPLIKHOPESEVGKIP--HLPHQASHSVTTRNDCKSP 222
QY 706 YORDIIRSNLSLPRMDVMH--SSVQTSLRERNNSLDGYVAVACQPPS----- 751
Db 223 HL--TVSSTNTLRSMPLHRAVVFHPRINHSLERKEGSS--SLSPFTLPVWPVYAGKV 279
QY 752 ---EBRTVPLRPBPGHLKTSCEBQIRKRPDQW-----AQYHTOK-----AP 791
Db 280 QSQKRPPLIPBPKDQANFKSSSEQSL--TEMRRPNNLSKEKTEHWEKSSGKIQAA 336
QY 792 LVSTLPVATQSPTPSPSLFSDVPRADPSEBVSQTKFEEDHLSHSPWSCGTIGSCINAI 851
Db 337 MASVIVRPSSSTKTSMPAMQOLASKDVRSESSAGAHKTDCLKLAEGETGRI--ILPNV 394
QY 852 DSEPKDVIANSAVAMDLDGQDVKRRLV-HLFTQRTKEEDPIIFSPDGPILSKMGALSR 910
Db 395 NND--SVHTKSEKNPOAVSQSVPSVMAVNTMCTK--TDVITSAADTIVSSWSG---- 448
QY 911 SRTGYHTTDPVQATASQSGATKPIIS-----VSDYPRVYNAVDSRMSYGEATS 960
Db 449 SEVTSLSNLTILASTSECEVSSKSVQPAVAKQCEKCVSTTAPVTLAS-----SKTGSVVOP 504
QY 961 SAHYVERDRFITVLDLSGHRKHSSTGDLLELQQAANSLLIQRANALAMQKMSLDE 1020
Db 505 SSGFSG---TTDFIHLKHKHA-----ALAAQYVSSN--ASTETBNALKNQTLASLPL 553
QY 1021 GHMLTLNLKSEILERNGELQSDYTEDATQTPRDRDIELELSAL-----DTDEPDAQ 1072
Db 554 DSTVICSTINKANSVANGQA-----SGTQSPNHTTKLKAMWLTHSSEDKNTNKGNS 606
QY 1073 SEPIEEL-----DIQGISQ-----NDQLN-----GMA 1098
Db 607 GNSVSEIIRKPSVNLIASTSDIQNSVDSKIIIVDKVYKVRRAKRTYESGESGSDS 666
QY 1099 VENGHPVOQHOKEPKK---QKKOS 1119
Db 667 DESEKSEQRTKRPKPYKKON 690

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RESULT 9
US-10-953-349-13469
; Sequence 13469, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13469
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-13469

Query Match          2.6%; Score 158.5; DB 6; Length 443;
Best Local Similarity 21.5%; Pred. No. 0.054;
Matches 104; Conservative 42; Mismatches 154; Indels 183; Gaps 22;

QY 434 AHSELEKYRLRNKKINATVTFPLLNKVGNNVTYTTAGNVISVIGSTETTGKIVPST 493
DB 67 AETQKELAKQLAQKSSS-----SS 87
QY 494 NGISNAENVSQLISRSTDTSLRALETYKVGKVGANGQ-----NAAGPSA 539
DB 88 HSQSNENRSPPTTDPKKTDNA-----SDANNQALALPHQIAPOQPAAPSA 135
QY 540 DSVTENKIGSP-----PKTPVSNVAATSAGPSN---VGTILNSVPQKSSPFLTRVPY 589
DB 136 QAAASNVTQAPQPPYIIPPTMPN-SALPHQHQNQLPSDOQYRTPLQVAPQPTPSQYT 194
QY 590 P-PHSENTIOYFQDPRPTQIPFEVPOYPTQGY-----YPP-----PTVPAGVAPCVR 635
DB 195 PSPPVQOQSHYQOPOQ--QOPPQQOQOQSOQVOPSPQPPMOSQVRPSSPNVYPPYQDN 252
QY 636 FVRSNNVPESSLPAPSMYPADHYSTFSPR--DRMNSSPY-----QPPPOPYGP 682
DB 253 --QATNPSPAETLPNSMAMQMPYSGVPPQGSNRADAIPTGYGAGRTVPQOQPPQMKSS 310
QY 683 VPPVSGMYAPYDSSRIWRPMPYQORDIIRNSNLPMDVMHSSVYQTSIRERYNSLDGY 742
DB 311 FPAPPGEMYGP-----TGSILPALPPPSA-----YMMYDGE 341
QY 743 YSVACQPPSEPR-----TTVPLPREPCGHLKTSCEQIRKRPD--QMAQYHTQKAPL 792
DB 342 GGRSHHPQPPPHPAQPGYPTPSASLQNPQGH-----NLMTANPNQSQFVRNHPYNELI 395
QY 793 VSTTLPVATQSTPPSPPLFSVDPRADFSSVSGTKFEE-----DHLSHYSP--- 838
DB 396 -----EKLVSNGFRGDHVASVI-QRNEBSGQAVDFNSVLDRLSSVGPORG 439
QY 839 -WS 840
DB 440 GWS 442

RESULT 10
US-10-953-349-13468
; Sequence 13468, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30

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; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13468
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-13468

Query Match          2.6%; Score 158.5; DB 6; Length 451;
Best Local Similarity 21.5%; Pred. No. 0.056;
Matches 104; Conservative 42; Mismatches 154; Indels 183; Gaps 22;

QY 434 AHSELEKYRLRNKKINATVTFPLLNKVGNNVTYTTAGNVISVIGSTETTGKIVPST 493
DB 75 AETQKELAKQLAQKSSS-----SS 95
QY 494 NGISNAENVSQLISRSTDTSLRALETYKVGKVGANGQ-----NAAGPSA 539
DB 96 HSQSNENRSPPTTDPKKTDNA-----SDANNQALALPHQIAPOQPAAPSA 143
QY 540 DSVTENKIGSP-----PKTPVSNVAATSAGPSN---VGTILNSVPQKSSPFLTRVPY 589
DB 144 QAAASNVTQAPQPPYIIPPTMPN-SALPHQHQNQLPSDOQYRTPLQVAPQPTPSQYT 202
QY 590 P-PHSENTIOYFQDPRPTQIPFEVPOYPTQGY-----YPP-----PTVPAGVAPCVR 635
DB 203 PSPPVQOQSHYQOPOQ--QOPPQQOQOQSOQVOPSPQPPMOSQVRPSSPNVYPPYQDN 260
QY 636 FVRSNNVPESSLPAPSMYPADHYSTFSPR--DRMNSSPY-----QPPPOPYGP 682
DB 261 --QATNPSPAETLPNSMAMQMPYSGVPPQGSNRADAIPTGYGAGRTVPQOQPPQMKSS 318
QY 683 VPPVSGMYAPYDSSRIWRPMPYQORDIIRNSNLPMDVMHSSVYQTSIRERYNSLDGY 742
DB 319 FPAPPGEMYGP-----TGSILPALPPPSA-----YMMYDGE 349
QY 743 YSVACQPPSEPR-----TTVPLPREPCGHLKTSCEQIRKRPD--QMAQYHTQKAPL 792
DB 350 GGRSHHPQPPPHPAQPGYPTPSASLQNPQGH-----NLMTANPNQSQFVRNHPYNELI 403
QY 793 VSTTLPVATQSTPPSPPLFSVDPRADFSSVSGTKFEE-----DHLSHYSP--- 838
DB 404 -----EKLVSNGFRGDHVASVI-QRNEBSGQAVDFNSVLDRLSSVGPORG 447
QY 839 -WS 840
DB 448 GWS 450

RESULT 11
US-10-953-349-13467
; Sequence 13467, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13467
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-13467

Query Match          2.6%; Score 158.5; DB 6; Length 456;
Best Local Similarity 21.5%; Pred. No. 0.057;
Matches 104; Conservative 42; Mismatches 154; Indels 183; Gaps 22;

QY 434 AHSELEKYRLRNKKINATVTFPLLNKVGNNVTYTTAGNVISVIGSTETTGKIVPST 493

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Db 80 AETQELAKLQLAQKSSSS-----SS 100
Qy 494 NGISNAEVSNSOLISRTSDSTLRALETVKVKGVKANGC-----MAAGPA 539
Db 101 HSQSNSEERSSPTTDPKKTDNA-----SDANNQALALAPHOIAPQPPAPAPSA 148
Qy 540 DSVTENKIGSP-----PKTPVSNVAATSAGPSN-----VGTSLNSVPOKSSPFLTRVPY 589
Db 149 QAAASNVTQAPQPPRYIIPPTMPN-SALPQHPOQYLPDSQOYRTPQVLAQPTPSQYT 207
Qy 590 P-PHSENIQYFODPRTQIPFEVQYPTQY-----YPP-----PTVPAGVAPCVPR 635
Db 208 PSPPVQGFSHYQOPOQO--QOPPOQOQOQWSQOVQPSQPPMQSGVRPSPVYPPYQPN 265
Qy 636 FVRSNNVPESSLPASMPADHYSTFSR--DRMNSSP-----QPPPOQYPR 682
Db 266 --QATNPSPAEITLPSMAMQMPYSGVPPQGSNRADAIPIGYGAGRTVPOQPPQMKSS 323
Qy 683 VPPVSGMYAPYDSSRRIRWPRMYQRDDIIRNSNLPAMDVHSSVYQTSLRERYSLDGY 742
Db 324 PPARPGEMGP-----TGSILPALPPSSA-----YMMYDGE 354
Qy 743 YSVACOPSESPR-----TTVPLPREPCGHLKTSCEQIRKPD--QMAQYHTQKADL 792
Db 355 GGRSHHPQPPHFAQPGYPTPSASLQNPQGH-----NLWVRNPQSQFVRNHPYNELI 408
Qy 793 VSTLPVATQSPPTPSPLFVSDFRADFSVSQTKFE-----DHLSHYSP-- 838
Db 409 -----EKLVSMTGFGDHVASVI--QRMESGQAVDFNSVLDRLSVGPORG 452
Qy 839 -WS 840
Db 453 GWS 455

RESULT 12
US-10-953-349-16346
; Sequence 16346, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16346
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-16346

Query Match 2.5%; Score 158; DB 6; Length 240;
Best Local Similarity 26.0%; Pred. No. 0.025;
Matches 73; Conservative 13; Mismatches 103; Indels 92; Gaps 14;

Qy 537 PSADSVTENKIGSPPKTPVSNVAATSAGPSNVGTSLNSVP--QKSPFLTRVPYPPHS 593
Db 17 PPPSPPTPYKXSPPPPYKXSPPPSPTPPYKXSPPPPYKXSPPPPKKHVHPY- 75
Qy 594 ENIQYQODRTOIPFEVQYPTQYPPPTVPAGVAPCVPRVRSNNVPESSLPASMP 653
Db 76 ---YHSPPPSPSPPPY---YKSP--PPSPSPPPPYHSPPPSPSP--P 122
Qy 654 YADHYSTFSRDRMNSSPYQPPPOPY---GPVPVPSGMYAPYDSSRRIRWPRMYQRDD 710
Db 123 YYYH---SP-----PPSPSPSPPYKXSPPPSPSP-----PPYYTQ-- 158
Qy 711 ITRSNLSPMDVHSSVYQTSLRERYSLDGYYSVACOPSESPRTTVPPLPREPCGHLKTS 770

Db 159 ---SPPPSPTRSHPPYYKS-----PP--PPTSYPSP----- 185
Qy 771 CEEQIRRKPDQMAQYH--TQKAPLVSTLPVATQSPPTSP 809
Db 186 -----PYHYVSPPPSPSPPPPYHYTSPPPSP 213

RESULT 13
US-10-505-928-799
; Sequence 799, Application US/10505928
; Publication No. US20060086532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505, 928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363, 019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 799
; LENGTH: 1384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-799

Query Match 2.5%; Score 153; DB 6; Length 1384;
Best Local Similarity 20.7%; Pred. No. 0.52;
Matches 158; Conservative 100; Mismatches 314; Indels 190; Gaps 32;

Qy 492 STNGISNAEVSNSOLISRTSDSTLRALETVKVKGVKANGQNAAGPSADSVTEN--KIG 548
Db 183 ATRGPS-ACASHSLVS-SIEKDQEIOMSLVEBPGAAGKKPAATSPSPMANGGRYLL 240
Qy 549 SPPKTPVSNVAATS-----AGPSNVGTSLNSVQKSSPFLTRVPYPPHSENIQ 597
Db 241 SPPTSPFGAMSVGSSYENTSPAFSPSPSPASGSCASHSPSGOEPGSPVPLVPARSSYH 300
Qy 598 YFODPRTQIP--FEVPOQYPTQYPPPT-----VPAGVAPCVPRFVRSNNVPE 644
Db 301 LALQPOSRPGARSBPRLSKKGHERPPGCLGLTDSPAATVLAAR--RATESR 358
Qy 645 --SSLPASMPYADHYST--FSRDRMNSSPYQPPPOPYGPVPPV--PSGMYAPY 695
Db 359 LGGQLPVVAISLSEVPASGALQPTSPGSKFQPVPAFKNKIGTLQORPSPFPREPG 418
Qy 696 DSRRIWRPMYQR-----DITRNSLPPMDVHSSVYQTSLRERYSLDGYYSVACQRP 750
Db 419 SRVLTSPSRQLVGRTFSDGLATRTLQPP-----SPRLGRGLD--SMRELPR 466
Qy 751 SEP-----RTVPLPREPCGHLKTSCEEQIRKPDQMAQYHTQKAPVSSTLPV---ATOS 803
Db 467 LSPSLSRRLALSPPTRTTTPDKLINREVAESbPRRMAA-HGASPEPFLTLGARGRRTS 525
Qy 804 PTPSPFLFSDVDRADFSVSQTKFEEDHLISHYSPWSCGTTGSCINALIDSEPRDIANSN 863
Db 526 PSFTLIGESLAPHKGSSGRLS--PAYGLGSLTGASFCQSPCVQKRLSGDLRVVTRERN 584
Qy 864 AVLMIDISGDVYKRVHLEFQRTKAEEDPIIPSPDGPIISKGAIRSSRTGHTHTDPQ 923
Db 585 SITEISDNEDDLLEVHRROERLREOE-----MERLRORELLETILNLIC 628
Qy 924 ATASQ-----GSATKPIISVDYVPVN-----AVDSRMSSYG- 955
Db 629 AEYSRADGPEAGELPISGEATPALLAARRRSPRGLAGASGSSSEPGVATQRLMESMER 688
Qy 956 -----NEATSSAHYVERDRFTVTLDSGRKHST--GDLISLE----- 991
Db 689 SDEENKKEGCSSTESTQOE-----HEDAPSTLQOEVALLEBRAOVGLAHVQLKV 739
Qy 992 -----LQAKSNLSLIQ--REANALAMQCKNMSLDEGRMLTINLSKELELN 1037

Db 740 RYKELEQQLQESAREAREMERALLQGERAREBRALLQKEQKAVDQ-----LQEKVLALET 792

Qy 1038 GELQSDYTEDA---TDYKPDREDI--LELSALDTEPD-----GQSEPIEF--- 1078

Db 793 G-LQKERDKEALAELETETLFEDELFQQLERESREVEERELAGQGLLRKASLELISIAKR 851

Qy 1079 -----ILDIQIQG-ISSQNDQLNGMAVENGHVPOQHQKEPK 1114

Db 852 KERLAILDSQAGQIRAOAVQESERILARDKNASLQILQKEKEK 893

RESULT 14

US-11-293-697-4492

/ Sequence 4492, Application US/11293697

/ Publication No. US20060105376A1

/ GENERAL INFORMATION:

/ APPLICANT: HELIX RESEARCH INSTITUTE

/ TITLE OF INVENTION: Novel full length cDNA

/ FILE REFERENCE: H1-A0106

/ CURRENT APPLICATION NUMBER: US/11/293,697

/ CURRENT FILING DATE: 2005-12-05

/ PRIOR APPLICATION NUMBER: US/10/108,260

/ PRIOR FILING DATE: 2002-03-28

/ NUMBER OF SEQ ID NOS: 5458

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 4492

/ LENGTH: 950

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-11-293-697-4492

Query Match 2.4%; Score 152; DB 7; Length 950;

Best Local Similarity 19.9%; Pred. No. 0.35;

Matches 178; Conservative 114; Mismatches 337; Indels 266; Gaps 44;

Qy 42 LNKLRKACPFDP-----QTALINDIDLVLPVNFALLOLVGQVPHQSIKLSNIGE--- 91

Db 109 VVKLQOEALDLELOMEKQKQETAGKQKELQIQAIDSL-DSIDPQSHMKAKQKSGKEQ 167

Qy 92 ---NKHYE-----VAKKCEDLALYLKPLSGKGVASINQSLSRPMQ----- 131

Db 168 LDYMKQYQQLSRDELISRIAKE-TEETKOLEBQLTGQIAAN---BALKKDLGCVIS 223

Qy 132 --RKVTLVNCQVBEQGVNRAARASIGERTVTELLIQHQNPQOLSLNMAAVARAC 189

Db 224 GLQEVLTGKQATQAKQNECRKLRDEKETLRLQTEV---EQRDLERL----- 269

Qy 190 QPLGPMQOEALQVLLALEDSALSRLVLFVQRLRPRFPQASKTISGHVQOLYRA 249

Db 270 ---VAMDAENNRKELAELE--SALOEO-----HEVNASLQQTQGLSAIYEALEEARL 316

Qy 250 SCFKVTKRDEDSLMQLKEEFSRYEALRR-----EHDQIVHIAM-ENGALRISPE 298

Db 317 NL-----RDMAEQKLEKELEKVTRLTQLEQSALQAELEKERRQALKNALGKAQSEEEK 369

Qy 299 QWSSLLYGDIAH-----KSHMQSIIDKQLQSPESFAKSVQELTIVLQ-RTG 342

Db 370 QENSELHAHLKHLQODNNLLKQQLKDFQNLHNVVDGLVRPEEVARVDELRRKLLGLTG 429

Qy 343 D-----PANTL-----NRLRPHLELLANTDPRNDVASPTWEQLENM-VAVKTVNHGLVD 390

Db 430 ENNIHSPSDVLKSLADLQKQFSEILARSKWERDEAQRERKLQOEMLAQOEKGLATGOE 489

Qy 391 FIO-----NYSRKGHETP-----OPQPNISKYKT 413

Db 490 FQQAQERALEARNMNDPKRQHEARIQOMENEIHYLOENLKSWEIQGLTLDLQGEADEEKE 549

Qy 414 SKCRDLRQGGCGPRGNTCTFAHQEE--LEKYLRLNKKINATRTFFPLANKYGVANNVT 470

Db 550 RLIALQLR---LEKKKLEDAKSQEQVFGIDKELKKLKAIVATSDKLATAEILLTAAQDLK 606

Qy 471 TTAGNVISV-----IGSTET-TGKIVPSTNGISNAENSVS--QLISRSTDSLRALET 520

Db 607 SLHGTVMKINGRAREBELOEAREFRSKRAQAARDLTRAEIELLOVLNRQKGBQFR-LEW 665

Qy 521 VKKGVKVGANGQMAAGPSADSVTENK-----IGSPKTPVSNVAATSG-PS 566

Db 666 EKTGVGTGANSQVLEIEIKENETMERQTEIARLQNLDTLGS DNKGFEENVLEIEILRR 725

Qy 567 NVGTELNSVQKQSPPLTRFVVPY---PHESENIQYFQDPRTO-----IPREVP- 611

Db 726 EVSQNDYISSNADDPKRGKGYWFMPPPSKVSSSHSCATQSGVGLKYSASTVPRKPR 785

Qy 612 ---QYFQTSYPPPT-----VPAGVAPCVF-RFVRS--NNVPSSU-----P 648

Db 786 PQQDQKSGSGPPRPAAGVWVYSPIRSGHLKLFPSNRADCGSGQSEELDDQEEPPFVP 845

Qy 649 PASMPPADHYSTFSPDRMNSP-----YQPPPPQP-----YGFVPVPSC 689

Db 846 PCYMWY-----TVLP---DGSFVQGMALYAPRPLPNNSRPLTGTIVVYGPFPAGAPM 896

Qy 690 MYAPVYDSRIRMPMYQRDILIRNSLP--PMDVHSSV---YQTSLERYNSL 739

Db 897 VYGP-----PPWF-----STFIPMGVLHCNVPEHHNLVSGKTYNSL 934

RESULT 15

US-10-953-349-21437

/ Sequence 21437, Application US/10953349

/ Publication No. US20060107345A1

/ GENERAL INFORMATION:

/ APPLICANT: ALEXANDROV, Nikolai et al.

/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

/ FILE REFERENCE: 2750-1579PUS2

/ CURRENT APPLICATION NUMBER: US/10/953,349

/ CURRENT FILING DATE: 2004-09-30

/ NUMBER OF SEQ ID NOS: 40252

/ SOFTWARE: PatentIn version 3.3

/ SEQ ID NO 21437

/ LENGTH: 343

/ TYPE: PRT

/ ORGANISM: Glycine max

US-10-953-349-21437

Query Match 2.4%; Score 151; DB 6; Length 343;

Best Local Similarity 23.6%; Pred. No. 0.099;

Matches 87; Conservative 32; Mismatches 131; Indels 118; Gaps 19;

Qy 535 AGPSADSVTENKIGSP-----PKTPVSNVAATSGAPSN--VGTELNSVPOKSSPFL 584

Db 31 AARPSQAASNTQAAPQPPYIIPTPMPN-SALRQHPQNOYLRPSDQYRTQLVAPQPT 89

Qy 585 RVVPYVP-PHESENIQYFQDPRTOIPREVPQYFQYGY-----YPP-----PTVPAGVA 630

Db 90 PQQVTPSPVQFQSHYQPOQ--QQPQQQQQQSQVQVQSPQPMQSVRPSBNVVP 147

Qy 631 PCVPRFVSNNTPESSLPASMPYADHYSTFPR--DRMNSSPY-----OPPP 677

Db 148 PYQPN--ATNPSPELTLPNSMAQMPYSGVPPQSGNRDALPYGVGAGRTVPQPPQ 205

Qy 678 QYGVVPVPVPSGMVYFVYDSRIRMPMYQRDILIRNSLPRMDVHSSVYQTSLERYN 737

Db 206 QMKSFAPRPGEMYG-----TSLPALPPSSA-----YM 236

Qy 738 SLDGYVVAQPPSPR-----TVVLPREPCGHLKTSCEEQIRRPD--QMAQYHT 787

Db 237 MYDGGGSGSHNRPQPPHFAQPGYPTTSASLQNPQGH-----NLAVRNPNQSQFVRNHP 290

Qy 788 QKAPLVSSTLVYATQSPFPSPPLFSDVDFRADSESYSCTKPR-----DHLSHY 836

Db 291 YNELI-----EKLVSNGFRGDHVASVY-QRMESGQADVNSVLDRLSSV 334

Qy 837 SP-----WS 840

Db 335 GPQRGWS 342

Wed May 31 11:47:35 2006

us-10-619-992-2.rapbn

Page 10

Search completed: May 24, 2006, 12:53:48
Job time : 15 secs

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

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OM protein - protein search, using sw model

Run on: May 24, 2006, 12:48:59 ; Search time 299 Seconds
(without alignments)
6082.290 Million cell updates/sec

Title: US-10-619-992-2

Perfect score: 6215

Sequence: 1 MPVQAQWTFUSCPICVNE.....MSEDNDPLFKPVANGKMNVS 1191

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues

Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:*

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52: /EMC_Celerra_SIDS3/ptodata/2/paa/US607_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6215	100.0	1191	US-10-170-205E-31443	Sequence 31443, A
2	6215	100.0	1191	US-10-619-992-2	Sequence 2, Appl1
3	6215	100.0	1191	US-60-452-680-22109	Sequence 22109, A
4	6215	100.0	1191	US-60-453-050-13599	Sequence 13599, A
5	6215	100.0	1191	US-60-453-135-13599	Sequence 13599, A
6	6215	100.0	1191	US-60-466-412-13599	Sequence 13599, A
7	6207	99.9	1191	US-10-619-992-4	Sequence 4, Appl1
8	5880	94.6	1137	US-60-243-734-16	Sequence 16, Appl1
9	5525	88.9	1062	US-10-170-205E-29971	Sequence 29971, A
10	5525	88.9	1062	US-60-452-680-22108	Sequence 22108, A
11	5525	88.9	1062	US-60-453-050-13598	Sequence 13598, A
12	5525	88.9	1062	US-60-453-135-13598	Sequence 13598, A
13	5525	88.9	1062	US-60-466-412-13598	Sequence 13598, A
14	5463	88.2	1048	US-10-485-225-8	Sequence 8, Appl1
15	4416	71.1	869	US-09-488-725A-3499	Sequence 3499, Ap
16	4416	71.1	869	US-10-258-898A-3499	Sequence 3499, Ap
17	4416	71.1	869	US-10-286-897-3499	Sequence 3499, Ap
18	4066.5	65.4	812	US-09-488-725A-3500	Sequence 3500, Ap
19	4066.5	65.4	812	US-10-258-898A-3500	Sequence 3500, Ap
20	4066.5	65.4	812	US-10-286-897-3500	Sequence 3500, Ap
21	2685	43.2	1134	US-60-733-162-682	Sequence 114, App
22	2685	43.2	1134	US-60-710-726-114	Sequence 682, App
23	2681.5	43.1	1133	US-60-733-162-682	Sequence 114, App
24	2665.5	42.9	1132	PCT-US02-3445-47	Sequence 47, Appl
25	2665	42.9	1132	US-10-170-205E-7090	Sequence 7090, Ap
26	2665	42.9	1132	US-10-461-673-10443	Sequence 10443, A
27	2665	42.9	1132	US-60-452-680-20520	Sequence 20520, A
28	2106	33.9	421	PCT-US00-30653-280	Sequence 280, A
29	1712.5	27.6	627	US-60-243-734-15	Sequence 15, Appl
30	1712.5	27.6	627	US-60-262-095-6	Sequence 6, Appl
31	1593	25.6	306	US-09-488-725A-7071	Sequence 7071, Ap
32	1593	25.6	306	US-09-488-725A-7072	Sequence 7072, Ap
33	1593	25.6	306	US-10-258-898A-7071	Sequence 7071, Ap
34	1593	25.6	306	US-10-258-898A-7072	Sequence 7072, Ap
35	1593	25.6	306	US-10-286-897-7071	Sequence 7071, Ap
36	1593	25.6	306	US-10-286-897-7072	Sequence 7072, Ap
37	1538	24.7	739	US-60-167-217-9685	Sequence 9685, Ap
38	1538	24.7	739	US-09-614-150-24915	Sequence 24915, A
39	1538	24.7	739	US-09-614-150A-24915	Sequence 24915, A
40	1538	24.7	739	US-11-097-143-24915	Sequence 24915, A
41	1538	24.7	739	US-60-173-464-20563	Sequence 20563, A
42	1538	24.7	739	US-60-191-637-25016	Sequence 25016, A
43	1538	24.7	739	US-60-191-637-25016	Sequence 19706, A
44	1492.5	24.0	296	PCT-US00-30653-281	Sequence 281, App
45	886	14.3	195	US-09-758-461-704	Sequence 704, App

ALIGNMENTS

RESULT 1
US-10-170-205E-31443
; Sequence 31443, Application US/10170205E
; GENERAL INFORMATION:

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; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
; FILE REFERENCE: CL001381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 31443
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-170-205E-31443

Query Match      100.0%; Score 6215; DB 31; Length 1191;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MPEVQAQWTEFLSCPTCYNEFDENVHKPISLCSHTVCTCKLHKRKACPFDDTAINTD 60

QY 61 IDVLPVNFALDQVGAQVDPDHOSIKLSNIGENKHYEVAKKCYEDALALYKPLSGKGVAS 120
DB 61 IDVLPVNFALDQVGAQVDPDHOSIKLSNIGENKHYEVAKKCYEDALALYKPLSGKGVAS 120

QY 121 LMQSALSRMOKRLVTLVNCOLVEEGRVRAARAASLGERVTTELILQHONPOOLSANL 180
DB 121 LMQSALSRMOKRLVTLVNCOLVEEGRVRAARAASLGERVTTELILQHONPOOLSANL 180

QY 181 WAAVBARGCOFLGPAMQEBALKVLVLALEDGSLSRKVLVLFVQRLERFPQASTSIG 240
DB 181 WAAVBARGCOFLGPAMQEBALKVLVLALEDGSLSRKVLVLFVQRLERFPQASTSIG 240

QY 241 HVVOLLYRASCKRYTKRDESSIMQKKEFRSYEALRREHDAQIYHIAEAGLRISPQW 300
DB 241 HVVOLLYRASCKRYTKRDESSIMQKKEFRSYEALRREHDAQIYHIAEAGLRISPQW 300

QY 301 SSLVGLDLAHKSHMOSIIDKLOSPEFAKSVQELTIVLQRTGDPANLNRLPHLELLANI 360
DB 301 SSLVGLDLAHKSHMOSIIDKLOSPEFAKSVQELTIVLQRTGDPANLNRLPHLELLANI 360

QY 361 DENPDVAVSPTWEOLENAVAVKTVVHGLVDFIQNSRKSHETPOPOPSNKYKISMCRDUR 420
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QY 421 OQGGCGPRGNTCTPAHSQEBLEKRYLRNKKINATVTRTEPLLNKGVANNVTYTTAGNVISYI 480
DB 421 OQGGCGPRGNTCTPAHSQEBLEKRYLRNKKINATVTRTEPLLNKGVANNVTYTTAGNVISYI 480

QY 481 GSTETTGKIVPSTNGISNAENSVSOLISRTDSTLALFTVKKVGVANGONAGPSAD 540
DB 481 GSTETTGKIVPSTNGISNAENSVSOLISRTDSTLALFTVKKVGVANGONAGPSAD 540

QY 541 SYTENKIGSPKTPVSNVAATSGAPSNVGTSLNSVPQKSSPFLTRVPVYPHSENIQYQ 600
DB 541 SYTENKIGSPKTPVSNVAATSGAPSNVGTSLNSVPQKSSPFLTRVPVYPHSENIQYQ 600

QY 601 DPRTOIPEFVPOYPOGTGYPPPPPTPVAGVAPCVPRFVRSNNVPESLLPSPAMPYADHYST 660
DB 601 DPRTOIPEFVPOYPOGTGYPPPPPTPVAGVAPCVPRFVRSNNVPESLLPSPAMPYADHYST 660

QY 661 FSPBDMNNSPVOPPPPOPGVPVPVPSGMYAVVYSRRIWRPMMQORDIIRNSNLPM 720
DB 661 FSPBDMNNSPVOPPPPOPGVPVPVPSGMYAVVYSRRIWRPMMQORDIIRNSNLPM 720

QY 721 DVMHSSVYQTSLRERNYSLDGYYSVACOPSESEPTVPLPRBPCGHLKTSCEBOIRKRD 780
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QY 781 QMAQIHTQCAPLVYSTLPAVATOSPSPSPVSDPADPSESVSGTKFEEDHLSHYSPWS 840
DB 781 QMAQIHTQCAPLVYSTLPAVATOSPSPSPVSDPADPSESVSGTKFEEDHLSHYSPWS 840

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DB 841 CGTIGSCINADSEBKDYIANSNAVLMDLSDGVGRVHLFETQRTKEEDEIIFPSDGP 900

QY 901 IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISSVDYVPYVNAVDSRMSYGNATS 960
DB 901 IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISSVDYVPYVNAVDSRMSYGNATS 960

QY 961 SAHYVERPFIYTDLSGRKHSSTGDLISLEQAKNSLLQREANLAMOQKNSLDE 1020
DB 961 SAHYVERPFIYTDLSGRKHSSTGDLISLEQAKNSLLQREANLAMOQKNSLDE 1020

QY 1021 GRHLTLNLKSEIELRNGELQSDYEDATDTKPDIDIELELSALDPTDEPGOSEPIEEL 1080
DB 1021 GRHLTLNLKSEIELRNGELQSDYEDATDTKPDIDIELELSALDPTDEPGOSEPIEEL 1080

QY 1081 DIQIGISSQNDQLNGMAVENGHVQOHQKEPPKOKKOSLGEDHYILEEQKTLIPVTSCE 1140
DB 1081 DIQIGISSQNDQLNGMAVENGHVQOHQKEPPKOKKOSLGEDHYILEEQKTLIPVTSCE 1140

QY 1141 SQPLPVSTISNASCLEPITTSVSAGNLILKTHVSEDKNDFLKRVANGKWN 1191
DB 1141 SQPLPVSTISNASCLEPITTSVSAGNLILKTHVSEDKNDFLKRVANGKWN 1191

RESULT 2
US-10-619-992-2
; Sequence 2, Application US/10619992
; GENERAL INFORMATION:
; APPLICANT: Hefenelder, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seis, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene at
; FILE REFERENCE: 00-617-A
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/921,099
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-619-992-2

Query Match      100.0%; Score 6215; DB 36; Length 1191;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPEVQAQWTEFLSCPTCYNEFDENVHKPISLCSHTVCTCKLHKRKACPFDDTAINTD 60
DB 1 MPEVQAQWTEFLSCPTCYNEFDENVHKPISLCSHTVCTCKLHKRKACPFDDTAINTD 60

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DB 61 IDVLPVNFALDQVGAQVDPDHOSIKLSNIGENKHYEVAKKCYEDALALYKPLSGKGVAS 120

QY 121 LMQSALSRMOKRLVTLVNCOLVEEGRVRAARAASLGERVTTELILQHONPOOLSANL 180
DB 121 LMQSALSRMOKRLVTLVNCOLVEEGRVRAARAASLGERVTTELILQHONPOOLSANL 180

QY 181 WAAVBARGCOFLGPAMQEBALKVLVLALEDGSLSRKVLVLFVQRLERFPQASTSIG 240
DB 181 WAAVBARGCOFLGPAMQEBALKVLVLALEDGSLSRKVLVLFVQRLERFPQASTSIG 240

QY 241 HVVOLLYRASCKRYTKRDESSIMQKKEFRSYEALRREHDAQIYHIAEAGLRISPQW 300
DB 241 HVVOLLYRASCKRYTKRDESSIMQKKEFRSYEALRREHDAQIYHIAEAGLRISPQW 300

QY 301 SSLVGLDLAHKSHMOSIIDKLOSPEFAKSVQELTIVLQRTGDPANLNRLPHLELLANI 360

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Db      |||||
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Db      |||||
361 DPNPAVSPTWEQLENAMAVAKTVHGLVDFIONYSRKHEPTPOPOPNKYKXSMCRDLR 420
Qy      |||||
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Db      |||||
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Qy      |||||
481 GSTETGKIVPSTNGISNAENSVSOLISRTSTSTLTALETVKVKGVGANGONAAAPSAD 540
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Qy      |||||
541 SVTENKIGSPKTPVSNVATSAAGPSNVGTELNSVPQKSPFLTRVPVYPHSENIQYFQ 600
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601 DPTQIPFEVPOYPOTGYPPPTPVAGVAPCVPRFVRNNVPBESSLPASMPYADHYST 660
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Qy      |||||
661 FSPDRMNSSPYOPPPPOYPGPVPPVPSGMVAPVYDSRRIWPRPMTQORDIIRNSLPPM 720
Db      |||||
661 FSPDRMNSSPYOPPPPOYPGPVPPVPSGMVAPVYDSRRIWPRPMTQORDIIRNSLPPM 720
Qy      |||||
721 DVHSSVYQTSLRERNYSLDGYYSVACOPPESEPTTVPLPREPCGHLKTKSCBQIRKRD 780
Db      |||||
721 DVHSSVYQTSLRERNYSLDGYYSVACOPPESEPTTVPLPREPCGHLKTKSCBQIRKRD 780
Qy      |||||
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Db      |||||
781 QMAQYHTQKAPLVSSSTLPVATOSPTPPSPPLFSYVDFRADSESYSCTKEEDHLSHSPWS 840
Qy      |||||
841 CGTISGCIATIDSEPDVANSNAVLMDDSGDKRRVHLFETORTKXEDPIIPSDGP 900
Db      |||||
841 CGTISGCIATIDSEPDVANSNAVLMDDSGDKRRVHLFETORTKXEDPIIPSDGP 900
Qy      |||||
901 IISKWGAISRSSRTGYHTTDPVQATASOGSATKPIISVSDYVPVYNAVDSRWSSYGNATS 960
Db      |||||
901 IISKWGAISRSSRTGYHTTDPVQATASOGSATKPIISVSDYVPVYNAVDSRWSSYGNATS 960
Qy      |||||
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Db      |||||
961 SAHYVERDRFIYTDLSGHRKHSSTGDLISLELOQAKSNLILQREANALAMQKNMSLDE 1020
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Db      |||||
1021 GRHLTNTLSKTELRNGELQSDYTEDATDKPRDIELELSALDTDEPDGSEPIEEL 1080
Qy      |||||
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Db      |||||
1081 DIOLGISSQNDOLNGLMAVENGHVQOHQKEPKOKOSLGEDHVLLEBQKTLPTVSGF 1140
Qy      |||||
1141 SQPLPVISINASCPTTTSVSAGNLLKTRHVMSEKNDPLKPYANGKMYNS 1191
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RESULT 3

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US-60-452-680-22109
; Sequence 22109, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FaSTSeq for Windows Version 4.0

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; SEQ ID NO 22109
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-22109
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Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1191; Conservative 0;
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Db      1 MFVQAQWTEFLSCPIYNEFDENVHKKPISLCSHTVCTCLNKRKAQCPDQATINTD 60
Qy      61 IDVLVNFALLQVGAQVPDHQSIKLSNDENKHYEAVAKCYBDLALYKPLSGGQVNS 120
Db      61 IDVLVNFALLQVGAQVPDHQSIKLSNDENKHYEAVAKCYBDLALYKPLSGGQVNS 120
Qy      121 LMQSALSRPMOKRLTVLNVCOLVEEGRVRAARAARSLGERTYTELILQHPQOLSANL 180
Db      121 LMQSALSRPMOKRLTVLNVCOLVEEGRVRAARAARSLGERTYTELILQHPQOLSANL 180
Qy      181 WAAVBARCGQFLGPMQOEALKVLVLALEDGALSRLVLFVYQRLERFRPQASKTISG 240
Db      181 WAAVBARCGQFLGPMQOEALKVLVLALEDGALSRLVLFVYQRLERFRPQASKTISG 240
Qy      241 HVOQLLYRASCFKVTYKREDDSLMOLKEEFNSYEALRREHDAQIYHIAEAGLRISPEQW 300
Db      241 HVOQLLYRASCFKVTYKREDDSLMOLKEEFNSYEALRREHDAQIYHIAEAGLRISPEQW 300
Qy      301 SLLIGDGLAHKSHMOSIIDKLOSPESFASVOELTIVLORTGDPALNLRPHLELLANI 360
Db      301 SLLIGDGLAHKSHMOSIIDKLOSPESFASVOELTIVLORTGDPALNLRPHLELLANI 360
Qy      361 DPNPAVSPTWEQLENAMAVAKTVHGLVDFIONYSRKHEPTPOPOPNKYKXSMCRDLR 420
Db      361 DPNPAVSPTWEQLENAMAVAKTVHGLVDFIONYSRKHEPTPOPOPNKYKXSMCRDLR 420
Qy      421 OQGGCPRGNTCTFAHSGEELKRYLRANKKINATVTRFPLNKVGVNNYTTTGANVISYI 480
Db      421 OQGGCPRGNTCTFAHSGEELKRYLRANKKINATVTRFPLNKVGVNNYTTTGANVISYI 480
Qy      481 GSTETGKIVPSTNGISNAENSVSOLISRTSTSTLTALETVKVKGVGANGONAAAPSAD 540
Db      481 GSTETGKIVPSTNGISNAENSVSOLISRTSTSTLTALETVKVKGVGANGONAAAPSAD 540
Qy      541 SVTENKIGSPKTPVSNVATSAAGPSNVGTELNSVPQKSPFLTRVPVYPHSENIQYFQ 600
Db      541 SVTENKIGSPKTPVSNVATSAAGPSNVGTELNSVPQKSPFLTRVPVYPHSENIQYFQ 600
Qy      601 DPTQIPFEVPOYPOTGYPPPTPVAGVAPCVPRFVRNNVPBESSLPASMPYADHYST 660
Db      601 DPTQIPFEVPOYPOTGYPPPTPVAGVAPCVPRFVRNNVPBESSLPASMPYADHYST 660
Qy      661 FSPDRMNSSPYOPPPPOYPGPVPPVPSGMVAPVYDSRRIWPRPMTQORDIIRNSLPPM 720
Db      661 FSPDRMNSSPYOPPPPOYPGPVPPVPSGMVAPVYDSRRIWPRPMTQORDIIRNSLPPM 720
Qy      721 DVHSSVYQTSLRERNYSLDGYYSVACOPPESEPTTVPLPREPCGHLKTKSCBQIRKRD 780
Db      721 DVHSSVYQTSLRERNYSLDGYYSVACOPPESEPTTVPLPREPCGHLKTKSCBQIRKRD 780
Qy      781 QMAQYHTQKAPLVSSSTLPVATOSPTPPSPPLFSYVDFRADSESYSCTKEEDHLSHSPWS 840
Db      781 QMAQYHTQKAPLVSSSTLPVATOSPTPPSPPLFSYVDFRADSESYSCTKEEDHLSHSPWS 840
Qy      841 CGTISGCIATIDSEPDVANSNAVLMDDSGDKRRVHLFETORTKXEDPIIPSDGP 900
Db      841 CGTISGCIATIDSEPDVANSNAVLMDDSGDKRRVHLFETORTKXEDPIIPSDGP 900
Qy      901 IISKWGAISRSSRTGYHTTDPVQATASOGSATKPIISVSDYVPVYNAVDSRWSSYGNATS 960
Db      901 IISKWGAISRSSRTGYHTTDPVQATASOGSATKPIISVSDYVPVYNAVDSRWSSYGNATS 960

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QY 961 SAHYERDRFIVTDLISGRKHSSTGDLISLEIQAKSNLSLQREANALAMQOKNSLDE 1020
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QY 1021 GRHLTLNLISKEIELRNGELQSDYTEDATDTKPRDRIELESALDPTDEPDGQSEPIEIL 1080
DB 1021 GRHLTLNLISKEIELRNGELQSDYTEDATDTKPRDRIELESALDPTDEPDGQSEPIEIL 1080
QY 1081 DIQLGSSQNDOLLNGMAVENHHPVOQHOKKEPPKOKKOSLGEDHYILEBOKTILPVTSCF 1140
DB 1081 DIQLGSSQNDOLLNGMAVENHHPVOQHOKKEPPKOKKOSLGEDHYILEBOKTILPVTSCF 1140
QY 1141 SGPPLVVISNASCPLPITTSVSAGNLILKTHVASEDKNDPLKPVANGKWNVS 1191
DB 1141 SGPPLVVISNASCPLPITTSVSAGNLILKTHVASEDKNDPLKPVANGKWNVS 1191

```

RESULT 4

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US-60-453-050-13599
; Sequence 13599, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13599
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-13599

```

Query Match 100.0%; Score 6215; DB 49; Length 1191;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MPVQAQWTEFLSCPICYNEFDENVHKKPISLGCSTHTVCKTCLNKLHKAACPFDOIAINTD 60
DB 1 MPVQAQWTEFLSCPICYNEFDENVHKKPISLGCSTHTVCKTCLNKLHKAACPFDOIAINTD 60
QY 61 IDVLPNFNALLQVGAQVDPDHOSIKLSNKGKHYEVAKKCVEDLALYLKPLSGGKGVAS 120
DB 61 IDVLPNFNALLQVGAQVDPDHOSIKLSNKGKHYEVAKKCVEDLALYLKPLSGGKGVAS 120
QY 121 LNQSALSRPMQRKLVTLVNCQVVEEGRVYRAMPAAASLGERVTTELILQHONPOQLSANTL 180
DB 121 LNQSALSRPMQRKLVTLVNCQVVEEGRVYRAMPAAASLGERVTTELILQHONPOQLSANTL 180
QY 181 WAAVRAAGCOFLGAPAMQEBALKVILALDEGSLSRKVLVLFVQORLEPRFPQASTSIG 240
DB 181 WAAVRAAGCOFLGAPAMQEBALKVILALDEGSLSRKVLVLFVQORLEPRFPQASTSIG 240
QY 241 HAVQULLYRASCFKVTYTRDEDSLSMOLKEEFRSYEALRRHDAQIVIAEAGLRISPEQM 300
DB 241 HAVQULLYRASCFKVTYTRDEDSLSMOLKEEFRSYEALRRHDAQIVIAEAGLRISPEQM 300
QY 301 SSLLYVDLHAKSHMOSIIDKLOSPEFAKSVQELTIVLORTGDPANILRLPHLELLANI 360
DB 301 SSLLYVDLHAKSHMOSIIDKLOSPEFAKSVQELTIVLORTGDPANILRLPHLELLANI 360
QY 361 DPNPDVSPPTWQOLENANVAVKTVTHGLVDFIQNSRKGHETPOPOPSKYKTSWCRDLR 420
DB 361 DPNPDVSPPTWQOLENANVAVKTVTHGLVDFIQNSRKGHETPOPOPSKYKTSWCRDLR 420
QY 421 OGGGCGRGNTCTFAHGOEELKRLNKKINATVRFPLANKVGNVYTTTGANIVSYI 480
DB 421 OGGGCGRGNTCTFAHGOEELKRLNKKINATVRFPLANKVGNVYTTTGANIVSYI 480

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QY 481 GSTETTGKIVSTNGISNAENSVSOLISRSTDSLRALETVKVKGANGAAGPSAD 540
DB 481 GSTETTGKIVSTNGISNAENSVSOLISRSTDSLRALETVKVKGANGAAGPSAD 540
QY 541 SYTENKIGSPKTPVSNVAISAGPSNVGTENLSVPOKSSPLTLTVPYVPPHSENIQYRQ 600
DB 541 SYTENKIGSPKTPVSNVAISAGPSNVGTENLSVPOKSSPLTLTVPYVPPHSENIQYRQ 600
QY 601 DPTQIPREVPQYPOGTGYPPPEPTVAGVAPCVPRFVSNNVPESSLPASAPYADHYST 660
DB 601 DPTQIPREVPQYPOGTGYPPPEPTVAGVAPCVPRFVSNNVPESSLPASAPYADHYST 660
QY 661 FSPDRMNSSPYQPPPPQYGPVPPVPSGMYAVYDSRRIRWPMYQORDIIRNSLPPM 720
DB 661 FSPDRMNSSPYQPPPPQYGPVPPVPSGMYAVYDSRRIRWPMYQORDIIRNSLPPM 720
QY 721 DYMSSVYQTSIREXNYSIDGYVAVACQPRASPRITVPLPRECGHLKTSCEQIRKPD 780
DB 721 DYMSSVYQTSIREXNYSIDGYVAVACQPRASPRITVPLPRECGHLKTSCEQIRKPD 780
QY 781 QMAOYHTOKAPLVSTLPAVATOSPFPSPPLFVDFRADFSESVSQKFEEDHLSHYS PWS 840
DB 781 QMAOYHTOKAPLVSTLPAVATOSPFPSPPLFVDFRADFSESVSQKFEEDHLSHYS PWS 840
QY 841 CGTIGCINAIIDSEPKDVIANSNAVJMDLDSGDVKKRVHLFETQRTYKEDP1IPFSDGP 900
DB 841 CGTIGCINAIIDSEPKDVIANSNAVJMDLDSGDVKKRVHLFETQRTYKEDP1IPFSDGP 900
QY 901 IISKGAISRSSRTGYHTTDPVQATASQSAKPIISVSYVYVYVNAVDSRMSYNGEARS 960
DB 901 IISKGAISRSSRTGYHTTDPVQATASQSAKPIISVSYVYVYVNAVDSRMSYNGEARS 960
QY 961 SAHYERDRFIVTDLISGRKHSSTGDLISLEIQAKSNLSLQREANALAMQOKNSLDE 1020
DB 961 SAHYERDRFIVTDLISGRKHSSTGDLISLEIQAKSNLSLQREANALAMQOKNSLDE 1020
QY 1021 GRHLTLNLISKEIELRNGELQSDYTEDATDTKPRDRIELESALDPTDEPDGQSEPIEIL 1080
DB 1021 GRHLTLNLISKEIELRNGELQSDYTEDATDTKPRDRIELESALDPTDEPDGQSEPIEIL 1080
QY 1081 DIQLGSSQNDOLLNGMAVENHHPVOQHOKKEPPKOKKOSLGEDHYILEBOKTILPVTSCF 1140
DB 1081 DIQLGSSQNDOLLNGMAVENHHPVOQHOKKEPPKOKKOSLGEDHYILEBOKTILPVTSCF 1140
QY 1141 SGPPLVVISNASCPLPITTSVSAGNLILKTHVASEDKNDPLKPVANGKWNVS 1191
DB 1141 SGPPLVVISNASCPLPITTSVSAGNLILKTHVASEDKNDPLKPVANGKWNVS 1191

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RESULT 5

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US-60-453-135-13599
; Sequence 13599, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13599
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-13599

```

Query Match 100.0%; Score 6215; DB 49; Length 1191;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPVQAQWTEFLSCPICYNEFDENVHKKPISLGCSTHTVCKTCLNKLHKAACPFDOIAINTD 60

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Db      1 MPVQAAMQWTEFLSCPICYNEFDENHAKPISLGGSHTVCTCLNKRKACPFQDTAINTD 60
Qy      61 IDVLPVNFALLQVGAQVDPDHOSIKLSNIGENKHYEVAKKCVEDLALYLKPLSGKGVAS 120
Db      61 IDVLPVNFALLQVGAQVDPDHOSIKLSNIGENKHYEVAKKCVEDLALYLKPLSGKGVAS 120
Qy      121 LMQSALSRRMQRKLVTLVNCQVVEEGRVRAARAASLGERVTTELILQHONPOOLSANL 180
Db      121 LMQSALSRRMQRKLVTLVNCQVVEEGRVRAARAASLGERVTTELILQHONPOOLSANL 180
Qy      181 MAABARAGCOFLGPAMQEBALKVLALLALDGSALSRSKVLFVVOQLERFPQASTSIG 240
Db      181 MAABARAGCOFLGPAMQEBALKVLALLALDGSALSRSKVLFVVOQLERFPQASTSIG 240
Qy      241 HVVOLLYRASCFKVTKRDESSLMQKEEFREYALRREHDAQIVHIAEAGLRISPEQM 300
Db      241 HVVOLLYRASCFKVTKRDESSLMQKEEFREYALRREHDAQIVHIAEAGLRISPEQM 300
Qy      301 SLLYGDLAHSKHMOSIIDKQSPESFAKSVQELTIVLQRTGDPANLRLPHLELLANI 360
Db      301 SLLYGDLAHSKHMOSIIDKQSPESFAKSVQELTIVLQRTGDPANLRLPHLELLANI 360
Qy      361 DNPDAVSPPTMQLERAMAVAKTVVHGLVDFIONYSRKGEHTPOQPNRSKXTSMCRDLR 420
Db      361 DNPDAVSPPTMQLERAMAVAKTVVHGLVDFIONYSRKGEHTPOQPNRSKXTSMCRDLR 420
Qy      421 OGGGCRGNTCTFAHSQEBLEKYLANKKINATVTRFPLNKVGANNVTYTTAGNYSVI 480
Db      421 OGGGCRGNTCTFAHSQEBLEKYLANKKINATVTRFPLNKVGANNVTYTTAGNYSVI 480
Qy      481 GSTETTGKIVPSTNGISNAENSVSOLISRSTDTLPALETVKVKGVGANGONAAAPSAD 540
Db      481 GSTETTGKIVPSTNGISNAENSVSOLISRSTDTLPALETVKVKGVGANGONAAAPSAD 540
Qy      541 SVTENKIGSPKTPVSNVAATSAAGPSNVGTELNSVPQKSSPFLTRVPVYPHSENIQYFO 600
Db      541 SVTENKIGSPKTPVSNVAATSAAGPSNVGTELNSVPQKSSPFLTRVPVYPHSENIQYFO 600
Qy      601 DPTQOIPFEVPOYPQYGYPPPTVPAGVAPCVPRFVRNNVPESSLPPASMPYADHYST 660
Db      601 DPTQOIPFEVPOYPQYGYPPPTVPAGVAPCVPRFVRNNVPESSLPPASMPYADHYST 660
Qy      661 FSPRDRMNSPYQPPPOPYGYPPVPSGMATVYDSRIWRPMTQORDDIRSNSLPPM 720
Db      661 FSPRDRMNSPYQPPPOPYGYPPVPSGMATVYDSRIWRPMTQORDDIRSNSLPPM 720
Qy      721 DVMHSSVYQTSLRERNYSLDGYYSVACOPPESEPTTVPLPREPCGHLKTSCEQIRKXD 780
Db      721 DVMHSSVYQTSLRERNYSLDGYYSVACOPPESEPTTVPLPREPCGHLKTSCEQIRKXD 780
Qy      781 QMAQYHTQAKAPVSTLPAVATOSPPTPSEPLFSVDFRADSESVGTFKFEEDHLSHSPMS 840
Db      781 QMAQYHTQAKAPVSTLPAVATOSPPTPSEPLFSVDFRADSESVGTFKFEEDHLSHSPMS 840
Qy      841 CCTIGSCINAIDSEPKDVIANSNAVIMDLDSGDVKRRVHLFETORTKEEDPIIPSDGP 900
Db      841 CCTIGSCINAIDSEPKDVIANSNAVIMDLDSGDVKRRVHLFETORTKEEDPIIPSDGP 900
Qy      901 IISXKGAISRSRSTGHTTDPVOATASQSAATKPIISVSDYVPVYNAVDRMSYNGEATS 960
Db      901 IISXKGAISRSRSTGHTTDPVOATASQSAATKPIISVSDYVPVYNAVDRMSYNGEATS 960
Qy      961 SAHYVERDRFIYVTDLSGHRKHSSTGDLISLELOQAKNSGILLQREANALAMQKMSLDE 1020
Db      961 SAHYVERDRFIYVTDLSGHRKHSSTGDLISLELOQAKNSGILLQREANALAMQKMSLDE 1020
Qy      1021 GHHLTNLISKEIELRNGELOSDYTEDATDTKPRDRIEFLSALDTPDEPGOSEPIEELL 1080
Db      1021 GHHLTNLISKEIELRNGELOSDYTEDATDTKPRDRIEFLSALDTPDEPGOSEPIEELL 1080
Qy      1081 DIOLGISSONDOLINGMAVENGNHPVOQHOKPEPKOKKOSLGEDHVLIEOKTILPVTSCF 1140

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Db      1081 DIOLGISSONDOLINGMAVENGNHPVOQHOKPEPKOKKOSLGEDHVLIEOKTILPVTSCF 1140
Qy      1141 SQPLPVISINASCPLPITTSVSAAGNILLKTHVWSEKNDPLKPYANGKMNVS 1191
Db      1141 SQPLPVISINASCPLPITTSVSAAGNILLKTHVWSEKNDPLKPYANGKMNVS 1191

RESULT 6
US-60-466-412-13599
; Sequence 13599, Application us/60466412
; GENERAL INFORMATION:
; APPLICANT: CARGILE, Michele
; APPLICANT: TAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001466
; CURRENT APPLICATION NUMBER: US/60/466,412
; NUMBER OF SEQ ID NOS: 2003-04-30
; SOFTWARE: FASTSEQ for windows Version 4.0
; SEQ ID NO 13599
; LENGTH: 1191
; TYPE: PRN
; ORGANISM: Homo sapiens
US-60-466-412-13599

Query Match      100.0%; Score 6215; DB 49; Length 1191;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MPVQAAMQWTEFLSCPICYNEFDENHAKPISLGGSHTVCTCLNKRKACPFQDTAINTD 60
Db      1 MPVQAAMQWTEFLSCPICYNEFDENHAKPISLGGSHTVCTCLNKRKACPFQDTAINTD 60
Qy      61 IDVLPVNFALLQVGAQVDPDHOSIKLSNIGENKHYEVAKKCVEDLALYLKPLSGKGVAS 120
Db      61 IDVLPVNFALLQVGAQVDPDHOSIKLSNIGENKHYEVAKKCVEDLALYLKPLSGKGVAS 120
Qy      121 LMQSALSRRMQRKLVTLVNCQVVEEGRVRAARAASLGERVTTELILQHONPOOLSANL 180
Db      121 LMQSALSRRMQRKLVTLVNCQVVEEGRVRAARAASLGERVTTELILQHONPOOLSANL 180
Qy      181 MAABARAGCOFLGPAMQEBALKVLALLALDGSALSRSKVLFVVOQLERFPQASTSIG 240
Db      181 MAABARAGCOFLGPAMQEBALKVLALLALDGSALSRSKVLFVVOQLERFPQASTSIG 240
Qy      241 HVVOLLYRASCFKVTKRDESSLMQKEEFREYALRREHDAQIVHIAEAGLRISPEQM 300
Db      241 HVVOLLYRASCFKVTKRDESSLMQKEEFREYALRREHDAQIVHIAEAGLRISPEQM 300
Qy      301 SLLYGDLAHSKHMOSIIDKQSPESFAKSVQELTIVLQRTGDPANLRLPHLELLANI 360
Db      301 SLLYGDLAHSKHMOSIIDKQSPESFAKSVQELTIVLQRTGDPANLRLPHLELLANI 360
Qy      361 DNPDAVSPPTMQLERAMAVAKTVVHGLVDFIONYSRKGEHTPOQPNRSKXTSMCRDLR 420
Db      361 DNPDAVSPPTMQLERAMAVAKTVVHGLVDFIONYSRKGEHTPOQPNRSKXTSMCRDLR 420
Qy      421 OGGGCRGNTCTFAHSQEBLEKYLANKKINATVTRFPLNKVGANNVTYTTAGNYSVI 480
Db      421 OGGGCRGNTCTFAHSQEBLEKYLANKKINATVTRFPLNKVGANNVTYTTAGNYSVI 480
Qy      481 GSTETTGKIVPSTNGISNAENSVSOLISRSTDTLPALETVKVKGVGANGONAAAPSAD 540
Db      481 GSTETTGKIVPSTNGISNAENSVSOLISRSTDTLPALETVKVKGVGANGONAAAPSAD 540
Qy      541 SVTENKIGSPKTPVSNVAATSAAGPSNVGTELNSVPQKSSPFLTRVPVYPHSENIQYFO 600
Db      541 SVTENKIGSPKTPVSNVAATSAAGPSNVGTELNSVPQKSSPFLTRVPVYPHSENIQYFO 600
Qy      601 DPTQOIPFEVPOYPQYGYPPPTVPAGVAPCVPRFVRNNVPESSLPPASMPYADHYST 660
Db      601 DPTQOIPFEVPOYPQYGYPPPTVPAGVAPCVPRFVRNNVPESSLPPASMPYADHYST 660

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OY 661 FSPDRMNSSPYQPPPOPGYGVPPVPSGMYA PVDYSRRIWRPMYQORDDIIRSNLSLPM 720
    |||
Db 661 FSPDRMNSSPYQPPPOPGYGVPPVPSGMYA PVDYSRRIWRPMYQORDDIIRSNLSLPM 720
OY 721 DVMHSSVYQTSLRERNYSLDGYYSVACQPPSEPRITVPLPREPCGHLKTSCEBQIRKRD 780
    |||
Db 721 DVMHSSVYQTSLRERNYSLDGYYSVACQPPSEPRITVPLPREPCGHLKTSCEBQIRKRD 780
OY 761 QMAQHTQKAPLVSSSTLPVATQSPTRPSPLFSVDPRADSESISGTFEEDHLSHYSPMS 840
    |||
Db 761 QMAQHTQKAPLVSSSTLPVATQSPTRPSPLFSVDPRADSESISGTFEEDHLSHYSPMS 840
OY 841 CGTIGSCINAIDSEPKDVIANSNAVIMLMDISGDVYKRVHLFETQRTKEEDPIIPSDGP 900
    |||
Db 841 CGTIGSCINAIDSEPKDVIANSNAVIMLMDISGDVYKRVHLFETQRTKEEDPIIPSDGP 900
OY 901 IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISSVDYVPYVNAVDSRMSYGENEATS 960
    |||
Db 901 IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISSVDYVPYVNAVDSRMSYGENEATS 960
OY 961 SAHYVERDRFIYTDLSGHRKHSSTGDLLELOQA KSNLLLOREANALAMOQKMSLDE 1020
    |||
Db 961 SAHYVERDRFIYTDLSGHRKHSSTGDLLELOQA KSNLLLOREANALAMOQKMSLDE 1020
OY 1021 GRHLTLNLISKEIELRNGELQSDYTEDATDTKPRDRIEELSLALDDEPDGSEPIEEL 1080
    |||
Db 1021 GRHLTLNLISKEIELRNGELQSDYTEDATDTKPRDRIEELSLALDDEPDGSEPIEEL 1080
OY 1081 DIQLGISSQNDOLNMGAVENGHPVQOHQKEPPKQKQSLGEBDHYLLEBOKTILPVTSCF 1140
    |||
Db 1081 DIQLGISSQNDOLNMGAVENGHPVQOHQKEPPKQKQSLGEBDHYLLEBOKTILPVTSCF 1140
OY 1141 SGPPLPVSISNACCLPITTSVSAGNLLKTHVMSSEKNDLFLKPVANGKMNS 1191
    |||
Db 1141 SGPPLPVSISNACCLPITTSVSAGNLLKTHVMSSEKNDLFLKPVANGKMNS 1191

RESULT 7
US-10-619-992-4
; Sequence 4, Application US/10619992
; GENERAL INFORMATION:
; APPLICANT: Hefeneider, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seies, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/10/619,992
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/921,099
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1191
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-619-992-4

Query Match 99.9%; Score 6207; DB 36; Length 1191;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MPVQAAQWTEBLSCTPCYNEFDENHVKPISLGCSHTVCKTCLNKLHAKACPFQOTAINND 60
    |||
Db 1 MAVOAAQWTEBLSCTPCYNEFDENHVKPISLGCSHTVCKTCLNKLHAKACPFQOTAINND 60
OY 61 IDVLPNPALLQVGAQVPHOSIKLSNIGENGYEYAKKCVEDLALYIKPLSGGKGVAS 120
    |||
Db 61 IDVLPNPALLQVGAQVPHOSIKLSNIGENGYEYAKKCVEDLALYIKPLSGGKGVAS 120

121 LNQSALSRPMQRKLVTLVNCQVLEEGRVVRAMRAARSLGERTVTELLLOHNPOLSANL 180
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Db 121 LNQSALSRPMQRKLVTLVNCQVLEEGRVVRAMRAARSLGERTVTELLLOHNPOLSANL 180
    |||
OY 181 WAAVBARCGQFLGPMOEBALKVLLALLEDGALSARKVLYLVVORLERPFOASTSTIG 240
    |||
Db 181 WAAVBARCGQFLGPMOEBALKVLLALLEDGALSARKVLYLVVORLERPFOASTSTIG 240
OY 241 HVOVLLYRASCFKVRKDEDSLSMOLKEFRSYEARREHDAQIVHIAEAGLRISPEQM 300
    |||
Db 241 HVOVLLYRASCFKVRKDEDSLSMOLKEFRSYEARREHDAQIVHIAEAGLRISPEQM 300
OY 301 SLLYGLDLAKSHMSOIIDKLOSPESPAKSVOELTIVLQRTDPPANLRLPHLELLANI 360
    |||
Db 301 SLLYGLDLAKSHMSOIIDKLOSPESPAKSVOELTIVLQRTDPPANLRLPHLELLANI 360
OY 361 DNPDAVSPTEWQLENNAMAVATVVGVLDFQNSRKQHEPQOPNSKYKTSMCORDR 420
    |||
Db 361 DNPDAVSPTEWQLENNAMAVATVVGVLDFQNSRKQHEPQOPNSKYKTSMCORDR 420
OY 421 QQGGCPRGNTCTFAHSELEKYLRLNKKINATVTFPLNKKVGVNNTVTAGNVISVI 480
    |||
Db 421 QQGGCPRGNTCTFAHSELEKYLRLNKKINATVTFPLNKKVGVNNTVTAGNVISVI 480
OY 481 GSTETTGKIVPSTNGISNAENSVSOLISRSTDSITLPALETYKVKVKGANGONAGPSAD 540
    |||
Db 481 GSTETTGKIVPSTNGISNAENSVSOLISRSTDSITLPALETYKVKVKGANGONAGPSAD 540
OY 541 SYTENKIGSPKTPVSNVATASAGSNVGTETANSVPQKSPFLTRPVY PPHSENIQYQ 600
    |||
Db 541 SYTENKIGSPKTPVSNVATASAGSNVGTETANSVPQKSPFLTRPVY PPHSENIQYQ 600
OY 601 DPTQIPEFVPOYPOGTGYPPPTVPAGVAPCVPRFVRNNYBESSLPASMPYADHYST 660
    |||
Db 601 DPTQIPEFVPOYPOGTGYPPPTVPAGVAPCVPRFVRNNYBESSLPASMPYADHYST 660
OY 661 FSPDRMNSSPYQPPPOPGYGVPPVPSGMYA PVDYSRRIWRPMYQORDDIIRSNLSLPM 720
    |||
Db 661 FSPDRMNSSPYQPPPOPGYGVPPVPSGMYA PVDYSRRIWRPMYQORDDIIRSNLSLPM 720
OY 721 DVMHSSVYQTSLRERNYSLDGYYSVACQPPSEPRITVPLPREPCGHLKTSCEBQIRKRD 780
    |||
Db 721 DVMHSSVYQTSLRERNYSLDGYYSVACQPPSEPRITVPLPREPCGHLKTSCEBQIRKRD 780
OY 781 QMAQHTQKAPLVSSSTLPVATQSPTRPSPLFSVDPRADSESISGTFEEDHLSHYSPMS 840
    |||
Db 781 QMAQHTQKAPLVSSSTLPVATQSPTRPSPLFSVDPRADSESISGTFEEDHLSHYSPMS 840
OY 841 CGTIGSCINAIDSEPKDVIANSNAVIMLMDISGDVYKRVHLFETQRTKEEDPIIPSDGP 900
    |||
Db 841 CGTIGSCINAIDSEPKDVIANSNAVIMLMDISGDVYKRVHLFETQRTKEEDPIIPSDGP 900
OY 901 IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISSVDYVPYVNAVDSRMSYGENEATS 960
    |||
Db 901 IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISSVDYVPYVNAVDSRMSYGENEATS 960
OY 961 SAHYVERDRFIYTDLSGHRKHSSTGDLLELOQA KSNLLLOREANALAMOQKMSLDE 1020
    |||
Db 961 SAHYVERDRFIYTDLSGHRKHSSTGDLLELOQA KSNLLLOREANALAMOQKMSLDE 1020
OY 1021 GRHLTLNLISKEIELRNGELQSDYTEDATDTKPRDRIEELSLALDDEPDGSEPIEEL 1080
    |||
Db 1021 GRHLTLNLISKEIELRNGELQSDYTEDATDTKPRDRIEELSLALDDEPDGSEPIEEL 1080
OY 1081 DIQLGISSQNDOLNMGAVENGHPVQOHQKEPPKQKQSLGEBDHYLLEBOKTILPVTSCF 1140
    |||
Db 1081 DIQLGISSQNDOLNMGAVENGHPVQOHQKEPPKQKQSLGEBDHYLLEBOKTILPVTSCF 1140
OY 1141 SGPPLPVSISNACCLPITTSVSAGNLLKTHVMSSEKNDLFLKPVANGKMNS 1191
    |||
Db 1141 SGPPLPVSISNACCLPITTSVSAGNLLKTHVMSSEKNDLFLKPVANGKMNS 1191

RESULT 8
```



```

US-60-243-734-16
; Sequence 16, Application US/60243734
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: DRUG-METABOLIZING PHASE I PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO00932
; CURRENT APPLICATION NUMBER: US/60/243, 734
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: HUMAN
US-60-243-734-16

Query Match      94.6%; Score 5880; DB 47; Length 1137;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1136; Conservative 1; Mismatches 0; Indels 54; Gaps 3;

QY 1 MEVOAQMTEFLSCPICYNEFDENVAKPISLGCSHTVCKTKLHRAKACPEPDQAIINTD 60
DB 1 MEVOAQMTEFLSCPICYNEFDENVAKPISLGCSHTVCKTKLHRAKACPEPDQAIINTD 60
QY 61 IDVLVFNALLQLVGAQVBDHOSIKLSNGENKHYEVAKKCYEDIALYLKPLSGKGVAS 120
DB 61 IDVLVFNALLQLVGAQVBDHOSIKLSNGENKHYEVAKKCYEDIALYLKPLSGKGVAS 120
QY 121 INQSALSRMOKRLVTLVNCOLVEEGRVRAARAASLGERVTTELIIQHNPQOLSANL 180
DB 121 INQSALSRMOKRLVTLVNCOLVEEGRVRAARAASLGERVTTELIIQHNPQOLSANL 180
QY 181 MAAVARAGCOFIPGPAQOEALKLVLLALDEGSALSRKVLVLFVVOLEPRFOASTSIG 240
DB 181 MAAVARAGCOFIPGPAQOEALKLVLLALDEGSALSRKVLVLFVVOLEPRFOASTSIG 240
QY 241 HVVOLLVYRASCFFKVTKRDEDSIMQKEFRSYEALRREHDAQIVHIMEAGLRISPEQM 300
DB 241 HVVOLLVYRASCFFKVTKRDEDSIMQKEFRSYEALRREHDAQIVHIMEAGLRISPEQM 300
QY 301 SELLVGDLLAHKHMOSIIDLKQSPESFAKSVQELTIVLQRTDPAALNRLPHLELLANI 360
DB 301 SELLVGDLLAHKHMOSIIDLKQSPESFAKSVQELTIVLQRTDPAALNRLPHLELLANI 360
QY 361 DENPDVAVPTMEOLEENAMVAKTVVHGLVDFIIONYSRKGHETPOPOPSKRYKSMCRDR 420
DB 361 DENPDVAVPTMEOLEENAMVAKTVVHGLVDFIIONYSRKGHETPOPOPSKRYKSMCRDR 420
QY 421 OQGGCGRGNTCTFAHSELEKRYLRNKKINATVTRTFPLLNKGVANNVTAGNVISYI 480
DB 421 OQGGCGRGNTCTFAHSELEKRYLRNKKINATVTRTFPLLNKGVANNVTAGNVISYI 480
QY 481 GSTETTGKLVSTNGISNAENSVSOLISRSTDTLALATVKKVGVANGVANGVANGVANGV 540
DB 481 GSTETTGKLVSTNGISNAENSVSOLISRSTDTLALATVKKVGVANGVANGVANGVANGV 540
QY 541 SYTENKIGSPKTPVSNVATSAAGPANGTELSVQKSSPFLTRVPVYPVPHSENIQYQ 600
DB 541 SYTENKIGSPKTPVSNVATSAAGPANGTELSVQKSSPFLTRVPVYPVPHSENIQYQ 600
QY 601 DERTQIPFEVPOYPOTGYVPPPTVAVGAPCVPRFVRSNNVDESSLPPASMPYADHYST 660
DB 601 DERTQIPFEVPOYPOTGYVPPPTVAVGAPCVPRFVRSNNVDESSLPPASMPYADHYST 660
QY 661 FSPRDMNSSPYOPPPQPGVPVPVSGVYAVVYSRKIRWPMYQORDIILNSNLPV 720
DB 661 FSPRDMNSSPYOPPPQPGVPVPVSGVYAVVYSRKIRWPMYQORDIILNSNLPV 720
QY 721 DVHSSVYOTSLRERNSLDGYVVAQPPSEPRITVPLPREBCGLKTSCEBOIRKRD 780
DB 721 DVHSSVYOTSLRERNSLDGYVVAQPPSEPRITVPLPREBCGLKTSCEBOIRKRD 780
QY 781 DVHSSVYOTSLRERNSLDGYVVAQPPSEPRITVPLPREBCGLKTSCEBOIRKRD 780
DB 781 DVHSSVYOTSLRERNSLDGYVVAQPPSEPRITVPLPREBCGLKTSCEBOIRKRD 780

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QY 781 QMAOYHTOKAPLVSSSTLPAVATOSPPTPSPPLFSDVDRADPSESVSQTKFEEDHLSHYSPWS 840
DB 741 QMAOYHTOKAPLVSSSTLPAVATOSPPTPSPPLFSDVDRADPSESVSQTKFEEDHLSHYSPWS 800
QY 841 CGTISGCINAIIDSEPKDVANSNAVLMDSDGDVRRVLFETORRTKEEDPIIPSDGP 900
DB 801 CGTISGCINAIIDSEPKDVANSNAVLMDSDGDVRRVLFETORRTKEEDPIIPSDGP 860
QY 901 IISKWGAISRSSRTGYHTDPVQATASQGSATKPISSVSDYVYVNAVADRSMSSYNGEATS 960
DB 861 IISKWGAISRSSRTGYHTDPVQATASQGSATKPISSVSDYVYVNAVADRSMSSYNGEATS 920
QY 961 SAHYVERDRFITYTDLSGHAKSSTGDLSELOQAQKSNLLLOREANALAMQKXNSLDE 1020
DB 921 SAHYVE-----RKHSSTGDLSELOQAQKSNLLLOREANALAMQKXNSLDE 968
QY 1021 GRHLTLNLTSKEILERNGELQSDYEDATDTKPRDRIELELSALDTPEDGQSEPIEELI 1080
DB 969 GRHLTLNLTSKEILERNGE--SDYEDATDTKPRDRIELELSALDTPEDGQSEPIEELI 1026
QY 1081 DIQLGISQNDQLNGMAVENGHVPVQOHQKEPPKOKQSLGEDHVILEBQKTIIPVTSCEP 1140
DB 1027 DIQLGISQNDQLNGMAVENGHVPVQOHQKEPPKOKQSLGEDHVILEBQKTIIPVTSCEP 1086
QY 1141 SQPLPVYSINASCPIPTTSVSAKNILKTHVNSEDKNDLKVANKMNS 1191
DB 1087 SQPLPVYSINASCPIPTTSVSAKNILKTHVNSEDKNDLKVANKMNS 1137

RESULT 9
US-10-170-205E-29971
; Sequence 29971, Application US/10170205E
; GENERAL INFORMATION:
; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
; FILE REFERENCE: CLO01381
; CURRENT APPLICATION NUMBER: US/10/170, 209E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29971
; LENGTH: 1062
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-29971

Query Match      88.9%; Score 5529; DB 31; Length 1062;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 MOKRLVTLVNCOLVEEGRVRAARAASLGERVTTELIIQHNPQOLSANLMAAVARAGC 189
DB 1 MOKRLVTLVNCOLVEEGRVRAARAASLGERVTTELIIQHNPQOLSANLMAAVARAGC 60
QY 190 OFLGPAMOEALKLVLLALDEGSALSRKVLVLFVVOLEPRFOASTSIGHYVOLLVYR 249
DB 61 OFLGPAMOEALKLVLLALDEGSALSRKVLVLFVVOLEPRFOASTSIGHYVOLLVYR 120
QY 250 SCFKYTKRDEDSIMQKEFRSYEALRREHDAQIVHIMEAGLRISPEOWSSLLVGDILA 309
DB 121 SCFKYTKRDEDSIMQKEFRSYEALRREHDAQIVHIMEAGLRISPEOWSSLLVGDILA 180
QY 310 HKSHMOSIIDLKQSPESFAKSVQELTIVLQRTGDPANLRLPHLELLANIDBNPDVAVSP 369
DB 181 HKSHMOSIIDLKQSPESFAKSVQELTIVLQRTGDPANLRLPHLELLANIDBNPDVAVSP 240
QY 370 TWEOLENAMVAKTVVHGLVDFIIONYSRKGHETPOPOPSKRYKTSKCRDLROGGCPRGT 429
DB 241 TWEOLENAMVAKTVVHGLVDFIIONYSRKGHETPOPOPSKRYKTSKCRDLROGGCPRGT 300
QY 430 NCTFAHSGELEBKRYLRNKKINATVTRTFPLLNKGVANNVTAGNVISIGSTETTGKI 489

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Db  NCTFAHSGOELEKYLRLNKKINATVTRPFLNKGVGNNTVTTAGNVISVISTETGKI 360
Qy  490 VPSTNGISNAENSVGOLISRSSTDSLRALETYKKGKVGANGONAAAGPADSVTEKIGS 549
Db  361 VPSTNGISNAENSVGOLISRSSTDSLRALETYKKGKVGANGONAAAGPADSVTEKIGS 420
Qy  550 PKTVPVSNVAATSAGSNVGTELNSVPQKSSPFLTRVPVYPHSENIQYFODPRIOIPE 609
Db  421 PKTVPVSNVAATSAGSNVGTELNSVPQKSSPFLTRVPVYPHSENIQYFODPRIOIPE 480
Qy  610 VPQYPTQGYPPPPPTVPAGVACVPRFVSNVNPBESSLPASMPYADHSTSPRDRMS 669
Db  481 VPQYPTQGYPPPPPTVPAGVACVPRFVSNVNPBESSLPASMPYADHSTSPRDRMS 540
Qy  670 SPYQPPPPQYGPVPVPBGMTAPVYDSRRIRPMPYQORDDIIIRNSLPPMDVMHSSVYQ 729
Db  541 SPYQPPPPQYGPVPVPBGMTAPVYDSRRIRPMPYQORDDIIIRNSLPPMDVMHSSVYQ 600
Qy  730 TSLRERYNSLDGYSVACQPPSEPRITVLPREPCGHLKTSCEBOIRRKPDQMAQYHTQK 789
Db  601 TSLRERYNSLDGYSVACQPPSEPRITVLPREPCGHLKTSCEBOIRRKPDQMAQYHTQK 660
Qy  790 APLVSTLPLVATQSPPTPSPPLFSVDFRADFSBSVSGTKEEDHLSHYSPWSCGTIGSCIN 849
Db  661 APLVSTLPLVATQSPPTPSPPLFSVDFRADFSBSVSGTKEEDHLSHYSPWSCGTIGSCIN 720
Qy  850 AIDSEPKDVIANSNVAVLMDLSDGDKVRVHLPETQRTKEEDPIIPFSQGPITISKGAIS 909
Db  721 AIDSEPKDVIANSNVAVLMDLSDGDKVRVHLPETQRTKEEDPIIPFSQGPITISKGAIS 780
Qy  910 RSSRTGYHTTDPVQATASQGSATKPIISVSDYVPYVAVDSRMSVSYNEATSSAHYVERDR 969
Db  781 RSSRTGYHTTDPVQATASQGSATKPIISVSDYVPYVAVDSRMSVSYNEATSSAHYVERDR 840
Qy  970 FIVTDLSGHRKXSSSTDLLSLLEQAKSNSLLQREANALAMQKXNSLDEGRHLLTNLL 1029
Db  841 FIVTDLSGHRKXSSSTDLLSLLEQAKSNSLLQREANALAMQKXNSLDEGRHLLTNLL 900
Qy  1030 SKEIELRNGELOSDYTEDATDTKPRDIELELSALDTPDQSGSEIIEILDIOQLGISQ 1089
Db  901 SKEIELRNGELOSDYTEDATDTKPRDIELELSALDTPDQSGSEIIEILDIOQLGISQ 960
Qy  1090 NQOLNGMAVENGHPIVQHQKEPKQKXSLGSDHVIIEBQKTIILPVTSQSFQPLVVIS 1149
Db  961 NQOLNGMAVENGHPIVQHQKEPKQKXSLGSDHVIIEBQKTIILPVTSQSFQPLVVIS 1020
Qy  1150 NASCLPITTSVSAAGNLIILKTHVMSSEDKNDFLKVANGKXVNS 1191
Db  1021 NASCLPITTSVSAAGNLIILKTHVMSSEDKNDFLKVANGKXVNS 1062

RESULT 10
US-60-452-680-22108
; Sequence 22108, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/60/452,680
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22108
; LENGTH: 1062
; TYPE: PRF
; ORGANISM: Homo sapiens
US-60-452-680-22108

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Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy  130 MOKRLVTLVNCOLVEEBGRVVRMARARSIGETVTELLIOHNPOLSANLMAAVRARC 189
Db  1 MOKRLVTLVNCOLVEEBGRVVRMARARSIGETVTELLIOHNPOLSANLMAAVRARC 60
Qy  150 QFLGPAMQEBALKVLALLLEDGALSRLVLFVVQRLEPPRPOASKTISIGHVOLLVRA 249
Db  61 QFLGPAMQEBALKVLALLLEDGALSRLVLFVVQRLEPPRPOASKTISIGHVOLLVRA 120
Qy  250 SCFKYTKRDEDSLSMQLKEEFPYSALRREHAQIVHIMEGLAISPQWSSLLYGDIA 309
Db  121 SCFKYTKRDEDSLSMQLKEEFPYSALRREHAQIVHIMEGLAISPQWSSLLYGDIA 180
Qy  310 HKSMMOSIIDKLQSPESFAKSVQELTIYVQRTGDPANLRLAPHELLANIDPNDAVSP 369
Db  181 HKSMMOSIIDKLQSPESFAKSVQELTIYVQRTGDPANLRLAPHELLANIDPNDAVSP 240
Qy  370 TWEOLENMAVAVKTVVHGLVDFIQNYSRKGHETPQPNKYKTSWCRDLRQGGCPRGT 429
Db  241 TWEOLENMAVAVKTVVHGLVDFIQNYSRKGHETPQPNKYKTSWCRDLRQGGCPRGT 300
Qy  430 NCTFAHSGOELEKYLRLNKKINATVTRPFLNKGVGNNTVTTAGNVISVISTETGKI 489
Db  301 NCTFAHSGOELEKYLRLNKKINATVTRPFLNKGVGNNTVTTAGNVISVISTETGKI 360
Qy  490 VPSTNGISNAENSVGOLISRSSTDSLRALETYKKGKVGANGONAAAGPADSVTEKIGS 549
Db  361 VPSTNGISNAENSVGOLISRSSTDSLRALETYKKGKVGANGONAAAGPADSVTEKIGS 420
Qy  550 PKTVPVSNVAATSAGSNVGTELNSVPQKSSPFLTRVPVYPHSENIQYFODPRIOIPE 609
Db  421 PKTVPVSNVAATSAGSNVGTELNSVPQKSSPFLTRVPVYPHSENIQYFODPRIOIPE 480
Qy  610 VPQYPTQGYPPPPPTVPAGVACVPRFVSNVNPBESSLPASMPYADHSTSPRDRMS 669
Db  481 VPQYPTQGYPPPPPTVPAGVACVPRFVSNVNPBESSLPASMPYADHSTSPRDRMS 540
Qy  670 SPYQPPPPQYGPVPVPBGMTAPVYDSRRIRPMPYQORDDIIIRNSLPPMDVMHSSVYQ 729
Db  541 SPYQPPPPQYGPVPVPBGMTAPVYDSRRIRPMPYQORDDIIIRNSLPPMDVMHSSVYQ 600
Qy  730 TSLRERYNSLDGYSVACQPPSEPRITVLPREPCGHLKTSCEBOIRRKPDQMAQYHTQK 789
Db  601 TSLRERYNSLDGYSVACQPPSEPRITVLPREPCGHLKTSCEBOIRRKPDQMAQYHTQK 660
Qy  790 APLVSTLPLVATQSPPTPSPPLFSVDFRADFSBSVSGTKEEDHLSHYSPWSCGTIGSCIN 849
Db  661 APLVSTLPLVATQSPPTPSPPLFSVDFRADFSBSVSGTKEEDHLSHYSPWSCGTIGSCIN 720
Qy  850 AIDSEPKDVIANSNVAVLMDLSDGDKVRVHLPETQRTKEEDPIIPFSQGPITISKGAIS 909
Db  721 AIDSEPKDVIANSNVAVLMDLSDGDKVRVHLPETQRTKEEDPIIPFSQGPITISKGAIS 780
Qy  910 RSSRTGYHTTDPVQATASQGSATKPIISVSDYVPYVAVDSRMSVSYNEATSSAHYVERDR 969
Db  781 RSSRTGYHTTDPVQATASQGSATKPIISVSDYVPYVAVDSRMSVSYNEATSSAHYVERDR 840
Qy  970 FIVTDLSGHRKXSSSTDLLSLLEQAKSNSLLQREANALAMQKXNSLDEGRHLLTNLL 1029
Db  841 FIVTDLSGHRKXSSSTDLLSLLEQAKSNSLLQREANALAMQKXNSLDEGRHLLTNLL 900
Qy  1030 SKEIELRNGELOSDYTEDATDTKPRDIELELSALDTPDQSGSEIIEILDIOQLGISQ 1089
Db  901 SKEIELRNGELOSDYTEDATDTKPRDIELELSALDTPDQSGSEIIEILDIOQLGISQ 960
Qy  1090 NQOLNGMAVENGHPIVQHQKEPKQKXSLGSDHVIIEBQKTIILPVTSQSFQPLVVIS 1149
Db  961 NQOLNGMAVENGHPIVQHQKEPKQKXSLGSDHVIIEBQKTIILPVTSQSFQPLVVIS 1020
Qy  1150 NASCLPITTSVSAAGNLIILKTHVMSSEDKNDFLKVANGKXVNS 1191
Db  1021 NASCLPITTSVSAAGNLIILKTHVMSSEDKNDFLKVANGKXVNS 1062

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Query Match 88.9%; Score 5525; DB 49; Length 1062;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 11
 US-60-453-050-13598
 ; Sequence 13598, Application US/60453050
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: LUKE, May
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001457
 ; CURRENT APPLICATION NUMBER: US/60/453, 050
 ; CURRENT FILING DATE: 2003-03-10
 ; NUMBER OF SEQ ID NOS: 82762
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 13598
 ; LENGTH: 1062
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 US-60-453-050-13598

Query Match 88.9%; Score 5525; DB 49; Length 1062;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 MORKLTVLVNCOI VEEGRVRAARAISIGERTVTELLIOHONPOOLSANLMAA VARGC 189
 DB 1 MORKLTVLVNCOI VEEGRVRAARAISIGERTVTELLIOHONPOOLSANLMAA VARGC 60
 QY 190 OFLGPMOBEAL KVLVLALEDGSALS RKYLVLFVVORLEPRFPQASKTSGHVVOLLYRA 249
 DB 61 OFLGPMOBEAL KVLVLALEDGSALS RKYLVLFVVORLEPRFPQASKTSGHVVOLLYRA 120
 QY 250 SCFKYTKRDESSLMQKEEFSYEALRREHDAQIYHIMEAGLRISPQWSSLLYGDIA 309
 DB 121 SCFKYTKRDESSLMQKEEFSYEALRREHDAQIYHIMEAGLRISPQWSSLLYGDIA 180
 QY 310 HXSHMOSIIDKLOSPSPFAKSVQELTIVLQRTGDPANLRLRPHLELANIDNPDAVSP 369
 DB 181 HXSHMOSIIDKLOSPSPFAKSVQELTIVLQRTGDPANLRLRPHLELANIDNPDAVSP 240
 QY 370 TWEOLENAMVA KTVVHGVLDFI QNYSRKGHETPOQPNSKYKTSMCRDLRQGGCPRGT 429
 DB 241 TWEOLENAMVA KTVVHGVLDFI QNYSRKGHETPOQPNSKYKTSMCRDLRQGGCPRGT 300
 QY 430 NCTFAHSELEKRYLRNKKINATVTPPLNKGVNNVTAGNVISIGSTETTKI 489
 DB 301 NCTFAHSELEKRYLRNKKINATVTPPLNKGVNNVTAGNVISIGSTETTKI 360
 QY 490 VPSTNGISNAENSVSQILSRSTDSLRALETYKVKGVANGONGAAGPSADSVTEKIGS 549
 DB 361 VPSTNGISNAENSVSQILSRSTDSLRALETYKVKGVANGONGAAGPSADSVTEKIGS 420
 QY 550 PKTPVSNVAASAGSNVTGELNSVPOKSPFLTRVPYPPHSENIQYFQDPRTOIPRE 609
 DB 421 PKTPVSNVAASAGSNVTGELNSVPOKSPFLTRVPYPPHSENIQYFQDPRTOIPRE 480
 QY 610 VPQYQOTGYPPPTVPAVAPCVPRFVRSNNVPBESSLPASMPYADHSTSPRDRMS 669
 DB 481 VPQYQOTGYPPPTVPAVAPCVPRFVRSNNVPBESSLPASMPYADHSTSPRDRMS 540
 QY 670 SFYQPPPPQYGPVPVPSGMYAPVYDSRRIMRPMYQODDIIRNSLPRMDVMHSSVYQ 729
 DB 541 SFYQPPPPQYGPVPVPSGMYAPVYDSRRIMRPMYQODDIIRNSLPRMDVMHSSVYQ 600
 QY 730 TSLREYVNSLDGYSAACQPPSEPRRTTVLPRPGHLLTSCBEOIRRRPDMQAOYHTOK 789
 DB 601 TSLREYVNSLDGYSAACQPPSEPRRTTVLPRPGHLLTSCBEOIRRRPDMQAOYHTOK 660
 QY 790 APLVSLTFLVATQSPRPSPPLFSVDPRADFSSESCTKFEEDHLSHYSPWSCGTTIGSCIN 849
 DB 661 APLVSLTFLVATQSPRPSPPLFSVDPRADFSSESCTKFEEDHLSHYSPWSCGTTIGSCIN 720

QY 850 AIDSEPKVIANSNVAIAMDLDGDKRVYALFETORRTKEEDPIIFPSDGPITISKMGAT 909
 DB 721 AIDSEPKVIANSNVAIAMDLDGDKRVYALFETORRTKEEDPIIFPSDGPITISKMGAT 780
 QY 910 RSSRGYHTTDPVOATASQGSATKPIVSQDYPPYVNAVDSRWSSYGENEATSSAHYVERDR 969
 DB 781 RSSRGYHTTDPVOATASQGSATKPIVSQDYPPYVNAVDSRWSSYGENEATSSAHYVERDR 840
 QY 970 FIVTDLSGHRKHSSTGDLISLELOAKSN\$LLLOREANALAMQKNSLDEGRHLLTNLL 1029
 DB 841 FIVTDLSGHRKHSSTGDLISLELOAKSN\$LLLOREANALAMQKNSLDEGRHLLTNLL 900
 QY 1030 SKEIELRNGELOS DTEDATDPKPDRIELESALDTPDQSEPIEELIDQLGISQ 1089
 DB 901 SKEIELRNGELOS DTEDATDPKPDRIELESALDTPDQSEPIEELIDQLGISQ 960
 QY 1090 NDQLNGMAVENGHAPVOHQKPEPKQKOSLGEDHVIIEOKTILPVTSCFSQPLPVIS 1149
 DB 961 NDQLNGMAVENGHAPVOHQKPEPKQKOSLGEDHVIIEOKTILPVTSCFSQPLPVIS 1020
 QY 1150 NASCLPITTSVAGNLI LKTHVMSDDKNDPLKPVANGKXVNS 1191
 DB 1021 NASCLPITTSVAGNLI LKTHVMSDDKNDPLKPVANGKXVNS 1062

RESULT 12
 US-60-453-135-13598
 ; Sequence 13598, Application US/60453135
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: TAKOUBOVA, Olga
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001456
 ; CURRENT APPLICATION NUMBER: US/60/453, 135
 ; CURRENT FILING DATE: 2003-03-10
 ; NUMBER OF SEQ ID NOS: 82762
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 13598
 ; LENGTH: 1062
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 US-60-453-135-13598

Query Match 88.9%; Score 5525; DB 49; Length 1062;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 MORKLTVLVNCOI VEEGRVRAARAISIGERTVTELLIOHONPOOLSANLMAA VARGC 189
 DB 1 MORKLTVLVNCOI VEEGRVRAARAISIGERTVTELLIOHONPOOLSANLMAA VARGC 60
 QY 190 OFLGPMOBEAL KVLVLALEDGSALS RKYLVLFVVORLEPRFPQASKTSGHVVOLLYRA 249
 DB 61 OFLGPMOBEAL KVLVLALEDGSALS RKYLVLFVVORLEPRFPQASKTSGHVVOLLYRA 120
 QY 250 SCFKYTKRDESSLMQKEEFSYEALRREHDAQIYHIMEAGLRISPQWSSLLYGDIA 309
 DB 121 SCFKYTKRDESSLMQKEEFSYEALRREHDAQIYHIMEAGLRISPQWSSLLYGDIA 180
 QY 310 HXSHMOSIIDKLOSPSPFAKSVQELTIVLQRTGDPANLRLRPHLELANIDNPDAVSP 369
 DB 181 HXSHMOSIIDKLOSPSPFAKSVQELTIVLQRTGDPANLRLRPHLELANIDNPDAVSP 240
 QY 370 TWEOLENAMVA KTVVHGVLDFI QNYSRKGHETPOQPNSKYKTSMCRDLRQGGCPRGT 429
 DB 241 TWEOLENAMVA KTVVHGVLDFI QNYSRKGHETPOQPNSKYKTSMCRDLRQGGCPRGT 300
 QY 430 NCTFAHSELEKRYLRNKKINATVTPPLNKGVNNVTAGNVISIGSTETTKI 489
 DB 301 NCTFAHSELEKRYLRNKKINATVTPPLNKGVNNVTAGNVISIGSTETTKI 360
 QY 490 VPSTNGISNAENSVSQILSRSTDSLRALETYKVKGVANGONGAAGPSADSVTEKIGS 549

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Db 361 VSTNGISNAENSVQSLISRSTDSLRALETYKXGKVGANGQNAAGPADSVTEKIGS 420
Qy 550 PKRTPVSNVAATSAGSNVGTELNSVPQKSSPFLTRVPYPPHSENIQYFQDPRTOIPE 609
Db 421 PKRTPVSNVAATSAGSNVGTELNSVPQKSSPFLTRVPYPPHSENIQYFQDPRTOIPE 480
Qy 610 VQYQPTGYPPPPYPPVAGVAPCPVPRFVSNVNPBESSLPASMPYADHSTSPRDRMS 669
Db 481 VQYQPTGYPPPPYPPVAGVAPCPVPRFVSNVNPBESSLPASMPYADHSTSPRDRMS 540
Qy 670 SPYQPPPPQYGPVPPVPSGMYAPVYDSRRIMRPMYQDIDIIRNSLDPMDVMHSSVYQ 729
Db 541 SPYQPPPPQYGPVPPVPSGMYAPVYDSRRIMRPMYQDIDIIRNSLDPMDVMHSSVYQ 600
Qy 730 TSLREKYNLSDGYSAVACQPSSEPRITVLPREPCHLKTSCBEQIRRRPDMQAYHTQK 789
Db 601 TSLREKYNLSDGYSAVACQPSSEPRITVLPREPCHLKTSCBEQIRRRPDMQAYHTQK 660
Qy 790 APLVSTLPLVATQSPTRPSPLFSVDRADFSSESVSGTKFEEDHLSHYSPWSCGTTIGSCIN 849
Db 661 APLVSTLPLVATQSPTRPSPLFSVDRADFSSESVSGTKFEEDHLSHYSPWSCGTTIGSCIN 720
Qy 850 AIDSEPKDVIANSNAVLMDLSDGVKRRVHLEFQRTKEEDPIIFPSDGPITISKWGAIS 909
Db 721 AIDSEPKDVIANSNAVLMDLSDGVKRRVHLEFQRTKEEDPIIFPSDGPITISKWGAIS 780
Qy 910 RSRRTGYHTTDPVQATASQGSATKPIVSVDYVPYVNAVDSRMSYGENATSSAHYVERDR 969
Db 781 RSRRTGYHTTDPVQATASQGSATKPIVSVDYVPYVNAVDSRMSYGENATSSAHYVERDR 840
Qy 970 FIVTDLSGHRKHSSTGDLISLEIQAKSNSLLQREANALAMQKXNSLDEGHILTLNLI 1029
Db 841 FIVTDLSGHRKHSSTGDLISLEIQAKSNSLLQREANALAMQKXNSLDEGHILTLNLI 900
Qy 1030 SKEIERNELSDYEDATDTKPRDIELEISALTDDEPGQSEPIEELIDIQIGISSQ 1089
Db 901 SKEIERNELSDYEDATDTKPRDIELEISALTDDEPGQSEPIEELIDIQIGISSQ 960
Qy 1090 NQOLNGMAVENGHPIVQHQKEPPKOKKOSLGEDHYILEBOKTILPVTSQFSPPLVVIS 1149
Db 961 NQOLNGMAVENGHPIVQHQKEPPKOKKOSLGEDHYILEBOKTILPVTSQFSPPLVVIS 1020
Qy 1150 NASCLPITTSVSAAGNLIKTHVMSSEDKNDFLKPVANGKXVNS 1191
Db 1021 NASCLPITTSVSAAGNLIKTHVMSSEDKNDFLKPVANGKXVNS 1062

RESULT 13
US-60-466-412-13598
; Sequence 13598, Application US/60466412
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: MOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/60/466,412
; NUMBER OF SEQ ID NOS: 429241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13598
; LENGTH: 1062
; TYPE: PRF
; ORGANISM: Homo sapiens
US-60-466-412-13598

Query Match 88.9%; Score 5525; DB 49; Length 1062;
Best local Similarity 100.0%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 130 MQRKLTVLNVCOLVEEGRVRAARAASLGERTVTEILLOHONPOOLSANLMAAVRARGC 189
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Db 1 MQRKLTVLNVCOLVEEGRVRAARAASLGERTVTEILLOHONPOOLSANLMAAVRARGC 60
Qy 190 OFLGPAMOEALKVLVLLLEDSSALSRKVLVLFVVQRLBPPRPOASKTSGHVOLLYRA 249
Db 61 OFLGPAMOEALKVLVLLLEDSSALSRKVLVLFVVQRLBPPRPOASKTSGHVOLLYRA 120
Qy 250 SCFKYTKRDESDSLNQLKEEPRSYEARREHDAQIVHILAMEAGLRISPQWSSLYGDIA 309
Db 121 SCFKYTKRDESDSLNQLKEEPRSYEARREHDAQIVHILAMEAGLRISPQWSSLYGDIA 180
Qy 310 HXSHMOSIIDKLOQSPESFAKSVQELTIVLQRTGDPANLRLRPHLELANIDPNDAVSP 369
Db 181 HXSHMOSIIDKLOQSPESFAKSVQELTIVLQRTGDPANLRLRPHLELANIDPNDAVSP 240
Qy 370 TWEOLENAMVAVKTVVHGLVDFIQNYSRKGHTPOPOPNSKTKTSMCRDLROQGGCPRT 429
Db 241 TWEOLENAMVAVKTVVHGLVDFIQNYSRKGHTPOPOPNSKTKTSMCRDLROQGGCPRT 300
Qy 430 NCTFAHSGEBELKYLRLNKKINATVTRPEPLNKVGVNNTVTYAGNVISIGSTETTKI 489
Db 301 NCTFAHSGEBELKYLRLNKKINATVTRPEPLNKVGVNNTVTYAGNVISIGSTETTKI 360
Qy 490 VSTNGISNAENSVQSLISRSTDSLRALETYKXGKVGANGQNAAGPADSVTEKIGS 549
Db 361 VSTNGISNAENSVQSLISRSTDSLRALETYKXGKVGANGQNAAGPADSVTEKIGS 420
Qy 550 PKRTPVSNVAATSAGSNVGTELNSVPQKSSPFLTRVPYPPHSENIQYFQDPRTOIPE 609
Db 421 PKRTPVSNVAATSAGSNVGTELNSVPQKSSPFLTRVPYPPHSENIQYFQDPRTOIPE 480
Qy 610 VQYQPTGYPPPPYPPVAGVAPCPVPRFVSNVNPBESSLPASMPYADHSTSPRDRMS 669
Db 481 VQYQPTGYPPPPYPPVAGVAPCPVPRFVSNVNPBESSLPASMPYADHSTSPRDRMS 540
Qy 670 SPYQPPPPQYGPVPPVPSGMYAPVYDSRRIMRPMYQDIDIIRNSLDPMDVMHSSVYQ 729
Db 541 SPYQPPPPQYGPVPPVPSGMYAPVYDSRRIMRPMYQDIDIIRNSLDPMDVMHSSVYQ 600
Qy 730 TSLREKYNLSDGYSAVACQPSSEPRITVLPREPCHLKTSCBEQIRRRPDMQAYHTQK 789
Db 601 TSLREKYNLSDGYSAVACQPSSEPRITVLPREPCHLKTSCBEQIRRRPDMQAYHTQK 660
Qy 790 APLVSTLPLVATQSPTRPSPLFSVDRADFSSESVSGTKFEEDHLSHYSPWSCGTTIGSCIN 849
Db 661 APLVSTLPLVATQSPTRPSPLFSVDRADFSSESVSGTKFEEDHLSHYSPWSCGTTIGSCIN 720
Qy 850 AIDSEPKDVIANSNAVLMDLSDGVKRRVHLEFQRTKEEDPIIFPSDGPITISKWGAIS 909
Db 721 AIDSEPKDVIANSNAVLMDLSDGVKRRVHLEFQRTKEEDPIIFPSDGPITISKWGAIS 780
Qy 910 RSRRTGYHTTDPVQATASQGSATKPIVSVDYVPYVNAVDSRMSYGENATSSAHYVERDR 969
Db 781 RSRRTGYHTTDPVQATASQGSATKPIVSVDYVPYVNAVDSRMSYGENATSSAHYVERDR 840
Qy 970 FIVTDLSGHRKHSSTGDLISLEIQAKSNSLLQREANALAMQKXNSLDEGHILTLNLI 1029
Db 841 FIVTDLSGHRKHSSTGDLISLEIQAKSNSLLQREANALAMQKXNSLDEGHILTLNLI 900
Qy 1030 SKEIERNELSDYEDATDTKPRDIELEISALTDDEPGQSEPIEELIDIQIGISSQ 1089
Db 901 SKEIERNELSDYEDATDTKPRDIELEISALTDDEPGQSEPIEELIDIQIGISSQ 960
Qy 1090 NQOLNGMAVENGHPIVQHQKEPPKOKKOSLGEDHYILEBOKTILPVTSQFSPPLVVIS 1149
Db 961 NQOLNGMAVENGHPIVQHQKEPPKOKKOSLGEDHYILEBOKTILPVTSQFSPPLVVIS 1020
Qy 1150 NASCLPITTSVSAAGNLIKTHVMSSEDKNDFLKPVANGKXVNS 1191
Db 1021 NASCLPITTSVSAAGNLIKTHVMSSEDKNDFLKPVANGKXVNS 1062

RESULT 14
US-10-485-225-8
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Sequence 8, Application US/10485225
; GENERAL INFORMATION:
; APPLICANT: Greener, Tsvika
; APPLICANT: Moskowitz, Haim
; APPLICANT: Reies, Yuval
; APPLICANT: Aliou, Iria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; MODULATION OF VIRAL MATURATION
; FILE REFERENCE: PROL-P02-001
; CURRENT APPLICATION NUMBER: US/10/485,225
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/308,958
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/345,846
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1048
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-225-8

Query Match      88.2%; Score 5483; DB 34; Length 1048;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPVQAQWTEFLSCPCVNEFDENVHKPISLGSHTVCTCKLHKRKAPEFDQTAINTD 60
DB 1 MPVQAQWTEFLSCPCVNEFDENVHKPISLGSHTVCTCKLHKRKAPEFDQTAINTD 60
QY 61 IDLFPVNFALLQVGAQVDPDHOSIKLSNIGENKHYEVAKKCYEDLALYKPLSGKGVAS 120
DB 61 IDLFPVNFALLQVGAQVDPDHOSIKLSNIGENKHYEVAKKCYEDLALYKPLSGKGVAS 120
QY 121 LNSQSLSPMOKKLVTVNVCQVVEEGRYRAMRARSIGERTVTEILLOHONPOOLSAVL 180
DB 121 LNSQSLSPMOKKLVTVNVCQVVEEGRYRAMRARSIGERTVTEILLOHONPOOLSAVL 180
QY 121 LNSQSLSPMOKKLVTVNVCQVVEEGRYRAMRARSIGERTVTEILLOHONPOOLSAVL 180
DB 121 LNSQSLSPMOKKLVTVNVCQVVEEGRYRAMRARSIGERTVTEILLOHONPOOLSAVL 180
QY 181 WAAVBARCGOFLGPMQOEALKVLVLALEDGSLSRKVLVLFVVOQLBEPFPOASTSIG 240
DB 181 WAAVBARCGOFLGPMQOEALKVLVLALEDGSLSRKVLVLFVVOQLBEPFPOASTSIG 240
QY 181 WAAVBARCGOFLGPMQOEALKVLVLALEDGSLSRKVLVLFVVOQLBEPFPOASTSIG 240
DB 181 WAAVBARCGOFLGPMQOEALKVLVLALEDGSLSRKVLVLFVVOQLBEPFPOASTSIG 240
QY 241 HVVQLLYRASCFKVTKRDESSLMQKEFRSYEALRREHDAQIVHIAEAGLRISPEQW 300
DB 241 HVVQLLYRASCFKVTKRDESSLMQKEFRSYEALRREHDAQIVHIAEAGLRISPEQW 300
QY 301 SSLLYGDLAHKSHMOSIIDKLOSPEFAKSVQELTIVLQRTGDPANLNRLPHLELANI 360
DB 301 SSLLYGDLAHKSHMOSIIDKLOSPEFAKSVQELTIVLQRTGDPANLNRLPHLELANI 360
QY 301 SSLLYGDLAHKSHMOSIIDKLOSPEFAKSVQELTIVLQRTGDPANLNRLPHLELANI 360
DB 301 SSLLYGDLAHKSHMOSIIDKLOSPEFAKSVQELTIVLQRTGDPANLNRLPHLELANI 360
QY 361 DPNPAVSPPTWQLENAMVAVKTVVHGLVDFIÖNSRKHEFTPOQPSNKYKTSMCRDLR 420
DB 361 DPNPAVSPPTWQLENAMVAVKTVVHGLVDFIÖNSRKHEFTPOQPSNKYKTSMCRDLR 420
QY 421 OQGGCPRGNTCTFAHSQEELEKYLRLNKKINATVTFPLLNKVGNNVTTTAGNVISVI 480
DB 421 OQGGCPRGNTCTFAHSQEELEKYLRLNKKINATVTFPLLNKVGNNVTTTAGNVISVI 480
QY 481 GSTETTGKIVPSTNGISNAENSVSOLISSTDSITLPALETIVKVGNGVANGONAGPSAD 540
DB 481 GSTETTGKIVPSTNGISNAENSVSOLISSTDSITLPALETIVKVGNGVANGONAGPSAD 540
QY 541 SVTENKIGSPPKTPVSNVAATAGPSNVGTIELNSVPQKSPFLTRPVVPHPSENIQYQ 600
DB 541 SVTENKIGSPPKTPVSNVAATAGPSNVGTIELNSVPQKSPFLTRPVVPHPSENIQYQ 600
QY 601 DPTQIPEFVPOYPOTGYYPPTPVAGYAPCVPRFVRSNNVPESGLPPASMPYADHYST 660
DB 601 DPTQIPEFVPOYPOTGYYPPTPVAGYAPCVPRFVRSNNVPESGLPPASMPYADHYST 660
QY 661 FSPRDRMNSSPQPPPOPYGPVPPVPSQMYAPVYDSRRIWPPMWQORDIIRNSLPPM 720
DB 661 FSPRDRMNSSPQPPPOPYGPVPPVPSQMYAPVYDSRRIWPPMWQORDIIRNSLPPM 720
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661 FSPRDRMNSSPQPPPOPYGPVPPVPSQMYAPVYDSRRIWPPMWQORDIIRNSLPPM 720
QY 721 DVMSSVYQTSILREYRNSLDGYYSVACOPPSPEPRTTVLPREPCHLTKSCGEQIRKRD 780
DB 721 DVMSSVYQTSILREYRNSLDGYYSVACOPPSPEPRTTVLPREPCHLTKSCGEQIRKRD 780
QY 781 OMAOYHTKAPVSSITLPATQSPTPPSPLFVVDPRADSESVSGTKFEEDHLSHSPMS 840
DB 781 OMAOYHTKAPVSSITLPATQSPTPPSPLFVVDPRADSESVSGTKFEEDHLSHSPMS 840
QY 841 CGTIGSCINAIIDSEKDYIANSNAVIMDLSDGVKRVHLPETORRTEKDEPIIPESDGP 900
DB 841 CGTIGSCINAIIDSEKDYIANSNAVIMDLSDGVKRVHLPETORRTEKDEPIIPESDGP 900
QY 901 IISKWGAISRSGRTGYHTTDPVQATASQGSATKPIVSVDYVYVNAVDSRMSYNGEATS 960
DB 901 IISKWGAISRSGRTGYHTTDPVQATASQGSATKPIVSVDYVYVNAVDSRMSYNGEATS 960
QY 961 SAHYVERDFITVTLDSGHRKSSSTDLLSLQQAQKNSLLQREANALAMQKNSLDE 1020
DB 961 SAHYVERDFITVTLDSGHRKSSSTDLLSLQQAQKNSLLQREANALAMQKNSLDE 1020
QY 1021 GRHLTLNLISKEIELRNGELQSDYTEDA 1048
DB 1021 GRHLTLNLISKEIELRNGELQSDYTEDA 1048

RESULT 15
US-09-488-725A-3499
; Sequence 3499, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hysq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 3495
; LENGTH: 870
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-3499

Query Match      71.1%; Score 4416; DB 24; Length 869;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 844; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 196 MOEALKVLVLALEDGSLSRKVLVLFVVOQLBEPFPOASTSIGHVVOLLYRASCFKXT 255
DB 1 MOEALKVLVLALEDGSLSRKVLVLFVVOQLBEPFPOASTSIGHVVOLLYRASCFKXT 255
QY 256 KDEDSSLMQKEFRSYEALRREHDAQIVHIAEAGLRISPEQWSSLLYGLAHKSHNQ 315
DB 256 KDEDSSLMQKEFRSYEALRREHDAQIVHIAEAGLRISPEQWSSLLYGLAHKSHNQ 315
QY 316 SIIDKLOSPEFAKSVQELTIVLQRTGDPANLNRLPHLELANIIDPNDAVSPWQLE 375
DB 316 SIIDKLOSPEFAKSVQELTIVLQRTGDPANLNRLPHLELANIIDPNDAVSPWQLE 375
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Db 121 SIIDLQSPESPAKSGVQELTIVLQRTGDPANLRLRPHLELLANIDPNDAVSPTEQLE 180
Qy 376 NAMVAVKTVVHGLVDFIQNYSRKGHETPQPNQSKYKTSMCRDLRQGGCPRGINTCFAN 435
Db 181 NAMVAVKTVVHGLVDFIQNYSRKGHETPQPNQSKYKTSMCRDLRQGGCPRGINTCFAN 240
Qy 436 SOEELKTRLRKKNATVTRFPPLNKVGNNTVTTAGNVISVIGSTETTKIVPSTNG 495
Db 241 SOEELKTRLRKKNATVTRFPPLNKVGNNTVTTAGNVISVIGSTETTKIVPSTNG 300
Qy 496 ISNAENSVSOLISRSTDSLRLALETVKKVKGANGQNAAGPSADSVTENKIGSPKTPV 555
Db 301 ISNAENSVSOLISRSTDSLRLALETVKKVKGANGQNAAGPSADSVTENKIGSPKTPV 360
Qy 556 SNVAATSAQPSNVGTELNVPQKSSPFLTRVPVYPHSENIOYFQDPRTQIPPEVPQYPO 615
Db 361 SNVAATSAQPSNVGTELNVPQKSSPFLTRVPVYPHSENIOYFQDPRTQIPPEVPQYPO 420
Qy 616 TGYPPPTVPAGVAPCVPRFVRNNVPPSSLPASMPYADHYSTPSPRDRMNSPYQPP 675
Db 421 TGYPPPTVPAGVAPCVPRFVRNNVPPSSLPASMPYADHYSTPSPRDRMNSPYQPP 480
Qy 676 PPQYGPVPVPVPSGMVAPYDSRRIRWPRMYORDIIRSNLSLPPMDVMHSSVYQTSLRER 735
Db 481 PPQYGPVPVPVPSGMVAPYDSRRIRWPRMYORDIIRSNLSLPPMDVMHSSVYQTSLRER 540
Qy 736 YNSLDGYVAVACQPPSEPRRTVPLPREPCGHLKTSCEBOIRRKPDQMAQYHTQKAPLVSS 795
Db 541 YNSLDGYVAVACQPPSEPRRTVPLPREPCGHLKTSCEBOIRRKPDQMAQYHTQKAPLVSS 600
Qy 796 TLPVATQSPPTPSPPLFSVDFRADFSESVSCTGKEEDHLSHYSPWSCGTIGSCINAIIDSEP 855
Db 601 TLPVATQSPPTPSPPLFSVDFRADFSESVSCTGKEEDHLSHYSPWSCGTIGSCINAIIDSEP 660
Qy 856 KQVIANSNVAVLMDLDSGDVYKRRVHLFETQRTKEEDPIIPFSDGPIISKWGAISRSSRTG 915
Db 661 KQVIANSNVAVLMDLDSGDVYKRRVHLFETQRTKEEDPIIPFSDGPIISKWGAISRSSRTG 720
Qy 916 YHTTDPVQATASQGSATKPIISVSDVYPYNAVDNRWSSYGNENATSSAHYVERDRFTVTDL 975
Db 721 YHTTDPVQATASQGSATKPIISVSDVYPYNAVDNRWSSYGNENATSSAHYVERDRFTVTDL 780
Qy 976 SGHRKHSSTGDDLSTLELQAKSNLSLLQREANALAMQKMSLDEGRHLTLNLSKEIEL 1035
Db 781 SGHRKHSSTGDDLSTLELQAKSNLSLLQREANALAMQKMSLDEGRHLTLNLSKEIEL 840
Qy 1036 RNGELQ 1041
Db 841 RNGEVK 846
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Search completed: May 24, 2006, 12:54:40
Job time : 301 secs